



## SEQUENCE LISTING

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Corixa Corporation

<120> Fusion Proteins of Mycobacterium Tuberculosis

<130> 014058-009041US

<140> US 09/688,672

<141> 2000-10-10

<150> US 60/158,338

<151> 1999-10-07

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<220>  
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<400> 7  
 tgttcttcga cggcaggctg gtggaggaag ggcccaccga acagctgttc tcctcgccga 60  
 agcatgccga aaccgcccga tacgtcgccg gactgtcggg ggacgtcaag gacgccaaagc 120  
 gcggaaattg aagagcacag aaaggtatgg cgtgaaaatt cgtttgcata cgctgttggc 180  
 cgtgttgacc gctgcgccgc tgctgctagc agcggcgggc tgtggctcga aaccaccgag 240  
 cggttcgccct gaaacggggc ccggcgccgg tactgtcgcg actacccccg cgtcgctgcc 300  
 ggtgacgttg gcggagaccg gtagcacgct gctctaccgc ctgttcaacc tgtgggggtcc 360  
 ggcttttcac gagaggtatc cgaacgtcac gatcaccgct cagggcaccg gttctgggtgc 420  
 cgggatcgcg caggccgccg ccgggacggt caacattggg gcctccgacg cctatctgtc 480  
 ggaaggtgat atggccgcgc acaaggggct gatgaacatc gcgctagcca tctccgctca 540  
 gcaggtcaac tacaacctgc ccggagttag cgagcacctc aagctgaacg gaaaagtcct 600  
 ggcgggccatg taccagggca ccatcaaaac ctgggacgac ccgcagatcg ctgcgctcaa 660  
 ccccggcgtg aacctgcccg gcaccgcggt agttccgctg caccgctccg acgggtccgg 720  
 tgacaccttc ttgttcaccc agtacctgtc caagcaagat cccgagggct ggggcaagtc 780  
 gcccggttc gccaccaccg tcgacttccc ggcggtgccg ggtgcgctgg gtgagaacgg 840  
 caacggcggc atggtgaccg gttgcgccga gacaccgggc tgcgtggcct atatcggcct 900  
 cagcttcctc gaccaggcca gtcaacgggg actcggcgag gcccaactag gcaatagctc 960  
 tggcaatttc ttgttgcccg acgcgcaaag cattcaggcg gcggcggtcg gcttcgcctc 1020  
 gaaaaccccc gcgaaccagg cgatttcgat gatcgacggg cccgccccgg acggctaccc 1080  
 gatcatcaac tacgagtacg ccatcgtcaa caaccggcaa aaggacgccg ccaccgcgca 1140  
 gaccttgtag gcatttctgc actgggcatg caccgacggc aacaaggcct cgttcctcga 1200  
 ccaggttcat ttccagccgc tgccgcccgc ggtggtgaag ttgtctgacg cgttgatcgc 1260  
 gacgatttcc agctagcctc gttgaccacc acgcgacagc aacctccgtc gggccatcgg 1320

```

gctgctttgc ggagcatgct ggcccgtgcc ggtgaagtcg gccgcgctgg cccggccatc 1380
cgggtggttg gtgggatagg tgcggtgata ccgctgcttg cgctggtctt ggtgctggtg 1440
gtgctgggtca tcgaggcgat ggggtgcgatc aggtcacaac ggttgcatctt cttcaccgcc 1500
accgaatgga atccaggcaa cacctacggc gaaaccgttg tcaccgacgc gtcgcccac 1560
cggtcggcgc ctactacggg gcgttgccgc tgatcgctcg gacgctggcg acctcgga 1620
tcgccctgat catcgcggtg ccggtctctg taggagcggc gctgggtgatc gtggaacggc 1680
tgccgaaacg gttggccgag gctgtgggaa tagtcctgga attgctcgcc ggaatcccca 1740
gcgtggtcgt cggtttgtgg ggggcaatga cgttcgggcc gttcatcgct catcacatcg 1800
ctccggtgat cgctcacaac gctcccgatg tgccggtgct gaactacttg cgcggcgacc 1860
cgggcaacgg ggagggcatg ttggtgtccg gtctggtgtt ggcggtgatg gtcgttccca 1920
ttatcgccac caccatcat gacctgttcc ggcaggtgcc ggtgttgccc cgggagggcg 1980
cgatcgggaa ttc
1993

```

```

<210> 8
<211> 374
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> 38kD

```

```

<400> 8
Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
  1             5             10             15

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
      20             25             30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
  35             40             45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
  50             55             60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
  65             70             75             80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
      85             90             95

Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
  100             105             110

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
  115             120             125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
  130             135             140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
  145             150             155             160

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
      165             170             175

Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
  180             185             190

Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
  195             200             205

```

Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly  
 210 215 220  
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu  
 225 230 235 240  
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala  
 245 250 255  
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn  
 260 265 270  
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe  
 275 280 285  
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro  
 290 295 300  
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn  
 305 310 315 320  
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu  
 325 330 335  
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val  
 340 345 350  
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu  
 355 360 365  
 Ile Ala Thr Ile Ser Ser  
 370

<210> 9  
 <211> 327  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb11 (Tb38-1)

<400> 9  
 cggcagcaga gaccgatgcc gctaccctcg cgcaggagggc aggtaatctc gagcggatct 60  
 ccggcgacct gaaaaccag atcgaccagg tggagtcgac ggcaggttcg ttgcagggcc 120  
 agtggcgcg cgcgcgggg acggccgccc aggcgcgggt ggtgcgcttc caagaagcag 180  
 ccaataagca gaagcaggaa ctgcagcaga tctgcagcaa tctcgtcag gccggcgctcc 240  
 aatactcgag ggccgacgag gacgacgagc aggcgctgtc ctgcgcaatg ggcttctgac 300  
 ccgctaatac gaaaagaaac ggagcaa 327

<210> 10  
 <211> 95  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb11 (Tb38-1)

```

<400> 10
Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1           5           10           15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
      20           25           30
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
      35           40           45
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
      50           55           60
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
      65           70           75           80
Ala Asp Glu Glu Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
      85           90           95

```

```

<210> 11
<211> 702
<212> DNA
<213> Mycobacterium tuberculosis

```

```

<220>
<223> TbH4

```

```

<220>
<221> modified_base
<222> (1)..(702)
<223> n = g, a, c or t

```

```

<400> 11
cggcacgagg atcgggtaccc cgcggcatcg gcagctgccg attcgccggg tttccccacc 60
cgaggaaagc cgctaccaga tggcgctgcc gaagtagggc gatccgttcg cgatgccggc 120
atgaacgggc ggcatacaat tagtgacaga acctttcagt ttagcgacga taatggctat 180
agcactaagg aggatgatcc gatatgacgc agtcgcagac cgtgacgggtg gatcagcaag 240
agattttgaa cagggccaac gaggtggagg ccccgatggc ggaccaccg actgatgtcc 300
ccatcacacc gtgcgaactc acgnggnta aaaacgccgc ccaacagntg gtnttgctcg 360
ccgacaacat gcgggaatac ctggcgggccg gtgccaaaga gcggcagcgt ctggcgacct 420
cgctgcgcaa cgcggccaag gngtatggcg aggttgatga ggaggctgcg accgcgctgg 480
acaacgacgg cgaaggaact gtgcaggcag aatcggccgg ggccgtcgga ggggacagtt 540
cggccgaact aaccgatacg ccgaggggtg ccacggccgg tgaacccaac ttcattggatc 600
tcaaagaagc ggcaaggaag ctcgaaacgg gcgaccaagg cgcacgctc gcgcactgng 660
gggatgggtg gaacacttnc accctgacgc tgcaaggcga cg 702

```

```

<210> 12
<211> 286
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> TbH4

```

```

<220>
<221> MOD_RES
<222> (1)..(286)
<223> Xaa = any amino acid

```

<400> 12

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val  
1 5 10 15

Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln  
20 25 30

His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val  
35 40 45

Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu  
50 55 60

Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe  
65 70 75 80

Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu  
85 90 95

Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala  
100 105 110

Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val  
115 120 125

Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp  
130 135 140

Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn  
145 150 155 160

Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg  
165 170 175

Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly  
180 185 190

Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile  
195 200 205

Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe  
210 215 220

Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp  
225 230 235 240

Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg  
245 250 255

Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln  
260 265 270

Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys  
275 280 285

<210> 13

<211> 1200

<212> DNA

<213> Mycobacterium tuberculosis

```

<400> 13
caggcatgag cagagcgttc atcatcgatc caacgatcag tgccattgac ggcttgtacg 60
accttctggg gattggaata cccaaccaag ggggtatcct ttactcctca ctagagtact 120
tcgaaaaaag cctggaggag ctggcagcag cgtttccggg tgatggctgg ttaggttcgg 180
ccgcggacaa atacgccggc aaaaaccgca accacgtgaa ttttttccag gaactggcag 240
acctcgatcg tcagctcatc agcctgatcc acgaccaggc caacgcggtc cagacgaccc 300
gcgacatcct ggagggcgcc aagaaaggtc tcgagttcgt gcgcccggtg gctgtggacc 360
tgacctacat cccggtcgtc gggcacgccc tatcgccgcg cttccaggcg ccgttttgcg 420
cgggcgcgat ggccgtagtg ggcggcgcgc ttgcctactt ggtcgtgaaa acgctgatca 480
acgcgactca actcctcaaa ttgcttgcca aattggcgga gttggtcgcg gccgccattg 540
cggacatcat ttcggatgtg gcggacatca tcaagggcac cctcggagaa gtgtgggagt 600
tcatcacaaa cgcgctcaac ggcctgaaag agctttggga caagctcacg ggggtgggtga 660
ccggactgtt ctctcgaggg tggtcgaacc tggagtcctt ctttgcgggc gtccccggct 720
tgaccggcgc gaccagcggc ttgtcgcaag tgactggcct gttcggtgcg gccggtctgt 780
ccgcacgcgc gggcttggct cacgcggata gcctggcgag ctcagccagc ttgcccgccc 840
tggccggcat tggggcgagg tccggttttg ggggcttgcc gagcctggct caggtccatg 900
ccgcctcaac tcggcaggcg ctacggcccc gagctgatgg cccggtcggc gccgctgccg 960
agcaggctcg cgggcagtcg cagctggtct ccgcgcaggg ttccaaggt atgggcggac 1020
ccgtaggcat gggcggcatg caccctctt cgggggcgtc gaaagggacg acgacgaaga 1080
agtactcgga aggcgcggcg gcgggcactg aagacgccga gcgcgcgcca gtcgaagctg 1140
acgcgggcgg tgggcaaaag gtgctggtac gaaacgtcgt ctaacggcat ggcgagccaa 1200

```

```

<210> 14
<211> 392
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> HTCC#1 (Mtb40)

```

```

<400> 14
Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
  1                      5                      10                      15

Leu Tyr Asp Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
      20                      25                      30

Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
      35                      40                      45

Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
      50                      55                      60

Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
      65                      70                      75                      80

Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
      85                      90                      95

Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
      100                     105                     110

Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
      115                     120                     125

Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
      130                     135                     140

Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
      145                     150                     155                     160

```



Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala  
 165 170 175  
 Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr  
 180 185 190  
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys  
 195 200 205  
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg  
 210 215 220  
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr  
 225 230 235 240  
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala  
 245 250 255  
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser  
 260 265 270  
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe  
 275 280 285  
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln  
 290 295 300  
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln  
 305 310 315 320  
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met  
 325 330 335  
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser  
 340 345 350  
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr  
 355 360 365  
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln  
 370 375 380  
 Lys Val Leu Val Arg Asn Val Val  
 385 390

<210> 15

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 (1-232)

<220>

<221> CDS

<222> (1)..(720)

<400> 15  
atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat cca 48  
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro  
1 5 10 15

acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata 96  
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile  
20 25 30

ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa 144  
Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys  
35 40 45

gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt 192  
Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly  
50 55 60

tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt 240  
Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe  
65 70 75 80

ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac 288  
Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His  
85 90 95

gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc 336  
Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala  
100 105 110

aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac 384  
Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr  
115 120 125

atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt 432  
Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe  
130 135 140

tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc 480  
Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val  
145 150 155 160

gtg aaa acg ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa 528  
Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys  
165 170 175

ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg 576  
Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val  
180 185 190

gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc aca 624  
Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr  
195 200 205

aac gcg ctc aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg tgg 672  
Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp  
210 215 220

gtg acc gga ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc taa 720  
 Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe  
 225 230 235 240

gaattc 726

<210> 16  
 <211> 239  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 (1-232)

<400> 16  
 Met His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro  
 1 5 10 15  
 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile  
 20 25 30  
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys  
 35 40 45  
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly  
 50 55 60  
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe  
 65 70 75 80  
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His  
 85 90 95  
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala  
 100 105 110  
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr  
 115 120 125  
 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe  
 130 135 140  
 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val  
 145 150 155 160  
 Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys  
 165 170 175  
 Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val  
 180 185 190  
 Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr  
 195 200 205  
 Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp  
 210 215 220  
 Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe  
 225 230 235

<210> 17  
 <211> 661  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1  
 (184-392)

<220>  
 <221> CDS  
 <222> (1)..(651)

```

<400> 17
atg cat cac cat cac cat cac gat gtg gcg gac atc atc aag ggc atc   48
Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile
   1             5             10             15

ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa   96
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
      20             25             30

gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga  144
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
      35             40             45

ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc  192
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
      50             55             60

ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc  240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
      65             70             75             80

ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc  288
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
      85             90             95

tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt  336
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
      100            105            110

ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg cag  384
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
      115            120            125

gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag  432
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln
      130            135            140

gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg  480
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
      145            150            155            160

ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg  528
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
      165            170            175

aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act  576
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr
      180            185            190

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gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa 624  
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln  
           195                          200                          205

aag gtg ctg gta cga aac gtc gtc taa cggcgaattc 661  
 Lys Val Leu Val Arg Asn Val Val  
           210                          215

<210> 18  
 <211> 216  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1  
           (184-392)

<400> 18  
 Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Ile  
       1                          5                          10                          15  
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys  
                           20                          25                          30  
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg  
           35                          40                          45  
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr  
       50                          55                          60  
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala  
       65                          70                          75                          80  
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser  
                           85                          90                          95  
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe  
           100                          105                          110  
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln  
           115                          120                          125  
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln  
       130                          135                          140  
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met  
       145                          150                          155                          160  
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser  
           165                          170                          175  
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr  
           180                          185                          190  
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln  
       195                          200                          205  
 Lys Val Leu Val Arg Asn Val Val  
       210                          215

<210> 19  
 <211> 411  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 (1-129)

<220>  
 <221> CDS  
 <222> (1)..(411)

<400> 19  
 atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat cca 48  
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro  
 1 5 10 15  
 acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata 96  
 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile  
 20 25 30  
 ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa 144  
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys  
 35 40 45  
 gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt 192  
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly  
 50 55 60  
 tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt 240  
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe  
 65 70 75 80  
 ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac 288  
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His  
 85 90 95  
 gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc 336  
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala  
 100 105 110  
 aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac 384  
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr  
 115 120 125  
 atc ccg gtc gtc ggg cac gcc cta tag 411  
 Ile Pro Val Val Gly His Ala Leu  
 130 135

<210> 20  
 <211> 136  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 (1-129)

<400> 20  
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro  
 1 5 10 15

Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile  
                   20                  25                  30  
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys  
                   35                  40                  45  
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly  
                   50                  55                  60  
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe  
                   65                  70                  75                  80  
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His  
                   85                  90                  95  
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala  
                   100                  105                  110  
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr  
                   115                  120                  125  
 Ile Pro Val Val Gly His Ala Leu  
                   130                  135

<210> 21  
 <211> 1225  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 (TM-1)

<220>  
 <221> CDS  
 <222> (4)..(1215)

<400> 21  
 cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat 48  
   Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp  
       1                  5                  10                  15  
 cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga 96  
 Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly  
                   20                  25                  30  
 ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa 144  
 Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu  
                   35                  40                  45  
 aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta 192  
 Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu  
                   50                  55                  60  
 ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat 240  
 Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn  
                   65                  70                  75  
 ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc 288  
 Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile  
                   80                  85                  90                  95

cac gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc	336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly	
100 105 110	
gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc	384
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr	
115 120 125	
tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg	432
Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro	
130 135 140	
ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt aag ctt gcc	480
Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala	
145 150 155	
tac ttg gtc gtg aaa acg ctg atc aac gcg aag ctt act caa ctc ctc	528
Tyr Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu	
160 165 170 175	
aaa ttg ctt gcc aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac	576
Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp	
180 185 190	
atc att tcg gat gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg	624
Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val	
195 200 205	
tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa gag ctt tgg gac	672
Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp	
210 215 220	
aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac	720
Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn	
225 230 235	
ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc	768
Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser	
240 245 250 255	
ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca	816
Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala	
260 265 270	
tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc tca gcc agc ttg	864
Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu	
275 280 285	
ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg	912
Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro	
290 295 300	
agc ctg gct cag gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc	960
Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro	
305 310 315	
cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag	1008
Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln	
320 325 330 335	



tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta 1056  
 Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val  
 340 345 350

ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg 1104  
 Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr  
 355 360 365

acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag 1152  
 Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu  
 370 375 380

cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta 1200  
 Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val  
 385 390 395

cga aac gtc gtc taa cggcgaattc 1225  
 Arg Asn Val Val  
 400

<210> 22  
 <211> 403  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 (TM-1)

<400> 22  
 Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro  
 1 5 10 15  
 Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile  
 20 25 30  
 Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys  
 35 40 45  
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly  
 50 55 60  
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe  
 65 70 75 80  
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His  
 85 90 95  
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala  
 100 105 110  
 Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr  
 115 120 125  
 Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe  
 130 135 140  
 Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Ala Tyr  
 145 150 155 160

Leu Val Val Lys Thr Leu Ile Asn Ala Lys Leu Thr Gln Leu Leu Lys  
 165 170 175  
 Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile  
 180 185 190  
 Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp  
 195 200 205  
 Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys  
 210 215 220  
 Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu  
 225 230 235 240  
 Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly  
 245 250 255  
 Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser  
 260 265 270  
 Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro  
 275 280 285  
 Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser  
 290 295 300  
 Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg  
 305 310 315 320  
 Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser  
 325 330 335  
 Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly  
 340 345 350  
 Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr  
 355 360 365  
 Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg  
 370 375 380  
 Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg  
 385 390 395 400  
 Asn Val Val

<210> 23

<211> 1225

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 (TM-2)

<220>

<221> CDS

<222> (4)..(1215)

<400> 23

cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat	48
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp	
1 5 10 15	
cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga	96
Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly	
20 25 30	
ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa	144
Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu	
35 40 45	
aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta	192
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu	
50 55 60	
ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat	240
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn	
65 70 75	
ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc	288
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile	
80 85 90 95	
cac gac cag gcc aac gcg gtc cag acg acc cgc gac aag ctt atc ctg	336
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu	
100 105 110	
gag ggc gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac	384
Glu Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp	
115 120 125	
ctg acc tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag	432
Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln	
130 135 140	
gcg ccg ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt gcc	480
Ala Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala	
145 150 155	
tac ttg gtc gtg aaa acg ctg atc aac gcg act caa ctc ctc aaa ttg	528
Tyr Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu	
160 165 170 175	
ctt gcc aaa ttg gcg gag ttg gtc gcg gcc gcc att gcg gac atc att	576
Leu Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile	
180 185 190	
tcg gat gtg gcg gac atc atc aag ggc atc ctc gga gaa gtg tgg gag	624
Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu	
195 200 205	
ttc atc aca aac gcg aag ctt ctc aac ggc ctg aaa gag ctt tgg gac	672
Phe Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp	
210 215 220	
aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga ggg tgg tcg aac	720
Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn	
225 230 235	

ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc ggc gcg acc agc	768
Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser	
240 245 250 255	
ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca	816
Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala	
260 265 270	
tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc tca gcc agc ttg	864
Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu	
275 280 285	
ccc gcc ctg gcc ggc att ggg ggc ggc tcc ggt ttt ggg ggc ttg ccg	912
Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro	
290 295 300	
agc ctg gct cag gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc	960
Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro	
305 310 315	
cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag	1008
Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln	
320 325 330 335	
tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta	1056
Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val	
340 345 350	
ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg	1104
Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr	
355 360 365	
acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag	1152
Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu	
370 375 380	
cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta	1200
Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val	
385 390 395	
cga aac gtc gtc taa cggcgaattc	1225
Arg Asn Val Val	
400	

<210> 24

<211> 403

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 (TM-2)

<400> 24

Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp Pro	
1 5 10 15	
Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile	
20 25 30	

Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys  
                   35                                  40                                  45  
 Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly  
           50                                  55                                  60  
 Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe  
   65                                  70                                  75                                  80  
 Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His  
                   85                                  90                                  95  
 Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Lys Leu Ile Leu Glu  
                   100                                  105                                  110  
 Gly Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu  
           115                                  120                                  125  
 Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala  
   130                                  135                                  140  
 Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr  
  145                                  150                                  155                                  160  
 Leu Val Val Lys Thr Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu  
                   165                                  170                                  175  
 Ala Lys Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser  
           180                                  185                                  190  
 Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe  
           195                                  200                                  205  
 Ile Thr Asn Ala Lys Leu Leu Asn Gly Leu Lys Glu Leu Trp Asp Lys  
   210                                  215                                  220  
 Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg Gly Trp Ser Asn Leu  
  225                                  230                                  235                                  240  
 Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly  
           245                                  250                                  255  
 Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser  
           260                                  265                                  270  
 Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro  
   275                                  280                                  285  
 Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser  
   290                                  295                                  300  
 Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg  
  305                                  310                                  315                                  320  
 Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser  
           325                                  330                                  335  
 Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly  
           340                                  345                                  350

Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr  
 355 360 365

Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg  
 370 375 380

Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg  
 385 390 395 400

Asn Val Val

<210> 25

<211> 3058

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> TbH9 (Mtb39A)

<400> 25

gatcgtagcc	gtgtagtg	tcgggcccgtt	tgaggatgga	gtgcacgtgt	ctttcgtgat	60
ggcataccca	gagatgttgg	cggcgccggc	tgacaccctg	cagagcatcg	gtgctaccac	120
tgtggctagc	aatgccgctg	cggcgccccc	gacgactggg	gtgggtgccc	ccgctgccga	180
tgagggtgctg	gcgctgactg	cggcgcaactt	cgccgcacat	gcggcgatgt	atcagtccgt	240
gagcgctcgg	gctgctgcga	ttcatgacca	gttcgtggcc	acccttgcca	gcagcgccag	300
ctcgtagtgcg	gccactgaag	tcgccaatgc	ggcgccggcc	agctaagcca	ggaacagtcg	360
gcacgagaaa	ccacgagaaa	tagggacacg	taatggtgga	tttcggggcg	ttaccaccgg	420
agatcaactc	cgcgaggatg	tacgcccggc	cgggttcggc	ctcgctggtg	gccgcccgtc	480
agatgtggga	cagcgtggcg	agtgacctgt	tttcggccgc	gtcggcggtt	cagtcgggtg	540
tctgggggtct	gacgggtggg	tcgtggatag	tttcgctcggc	gggtctgatg	gtggcgccgg	600
cctcgccgta	tgtggcggtg	atgagcgtca	ccgcggggca	ggccgagctg	accgcccggc	660
aggtccgggt	tgtgcccggc	gcctacgaga	cggcgtagtg	gctgacgggt	ccccgcggc	720
tgatcgccga	gaaccgtgct	gaactgatga	ttctgatagc	gaccaacctc	ttggggcaaa	780
acaccccggc	gatcgcggtc	aacgaggccg	aatacgccga	gatgtgggcc	caagacgccg	840
ccgcgatgtt	tggtacgccc	gcggcgacgg	cgacggcgac	ggcgacgttg	ctgccgttcg	900
aggaggcgcc	ggagatgacc	agcgcgggtg	ggctcctcga	gcaggccgcc	gcggtcagag	960
aggcctccga	caccgcggcg	gcgaaccagt	tgatgaacaa	tgtgccccag	gcgctgcaac	1020
agctggccca	gcccacgcag	ggcaccacgc	cttcttccaa	gctgggtggc	ctgtggaaga	1080
cgggtctcgcc	gcatcggtcg	ccgatcagca	acatggtgtc	gatggccaac	aaccacatgt	1140
cgatgaccaa	ctcgggtgtg	tcgatgacca	acaccttgag	ctcgatgttg	aagggtcttg	1200
ctccggcgcc	ggccgcccag	gccgtgcaaa	ccgcggcgca	aaacggggtc	cgggcgatga	1260
gtcgcgtggg	cagctcgctg	ggttcttcgg	gtctggggcg	tggggtggcc	gccaacttgg	1320
gtcggggcgg	ctcgggtcgg	tcgttgtcgg	tgccgcaggc	ctgggcccgc	gccaaccagg	1380
cagtcacccc	ggcggcgcgg	gcgctgccgc	tgaccagcct	gaccagcgcc	gcggaaagag	1440
ggcccgggca	gatgctgggc	gggctgccgg	tggggcagat	gggcgccagg	gccggtggtg	1500
ggctcagtg	tgtgctgcgt	gttcgcgcgc	gacctatgt	gatgccgcgt	tctccggcgg	1560
ccggctagga	gagggggcgc	agactgtcgt	tatttgacca	gtgatcggcg	gtctcggtgt	1620
ttccgcggcc	ggctatgaca	acagtcaatg	tgcatgacaa	gttacaggta	ttaggtccag	1680
gttcaacaag	gagacaggca	acatggcctc	acgttttatg	acggatccgc	acgcgatgcg	1740
ggacatggcg	ggccgttttg	aggtgcacgc	ccagacggtg	gaggacgagg	ctcgccggat	1800
gtgggcgtcc	gcgcaaaaca	tttcgggtgc	gggctggagt	ggcatggccg	aggcgacctc	1860
gctagacacc	atggcccaga	tgaatcaggc	gtttcgcaac	atcgtgaaca	tgctgcacgg	1920
ggtgcgtgac	gggctggttc	gcgacgcaa	caactacgag	cagcaagagc	aggcctccca	1980
gcagatcctc	agcagctaac	gtcagccgct	gcagcacaat	acttttataa	gcgaaggaga	2040
acagggttcga	tgaccatcaa	ctatcaattc	ggggatgtcg	acgctcacgg	cgccatgatc	2100
cgcgctcagg	ccgggttgct	ggaggccgag	catcaggcca	tcattcgtga	tgtgttgacc	2160
gcgagtgact	tttggggcgg	cgccggttcg	gcggcctgcc	aggggttcat	taccagttg	2220
ggccgtaact	tccaggtgat	ctacgagcag	gccaacgccc	acgggcagaa	ggtgcaggct	2280
gccggcaaca	acatggcgca	aaccgacagc	gccgtcggct	ccagctgggc	ctgacaccag	2340
gccaaggcca	gggacgtggt	gtacgagtga	agttcctcgc	gtgatccttc	gggtggcagt	2400

```

ctaagtggtc agtgctgggg tgttggtggt ttgctgcttg gcggggttctt cgggtgctggt 2460
cagtgcctgct cgggctcggg tgaggacctc gaggcccagg tagcgccgctc cttcgatcca 2520
ttcgtcgtgt tgttcggcga ggacgggtcc gacgaggcgg atgatcgagg cgcggtcggg 2580
gaagatgcc acgacgtcgg ttcggcgctg tacctctcgg ttgaggcggt cctggggggt 2640
gttgaccag atttggcgcc agatctgctt ggggaaggcg gtgaacgcca gcaggtcggt 2700
gcgggcggtg tcgagggtgct cggccaccgc ggggagtttg tcggtcagag cgtcgagtac 2760
ccgatcatat tgggcaacaa ctgattcggc gtcgggctgg tcgtagatgg agtgcagcag 2820
ggtgcgcacc cacggccagg agggcttcgg ggtggctgcc atcagattgg ctgcgtagt 2880
ggttctgcag cgctgccagg ccgctgcggg cagggtggcg ccgatcgcg ccaccaggcc 2940
ggcgtgggcg tcgctggtga ccagcgcgac cccggacagg ccgcgggcga ccaggtcgcg 3000
gaagaacgcc agccagccgg ccccgctctc ggcgagggtg acctggatgc ccaggatc 3058

```

<210> 26

<211> 391

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> TbH9 (Mtb39A)

<400> 26

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Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
  1                      5                      10                      15

Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
      20                      25                      30

Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
      35                      40                      45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
      50                      55                      60

Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
      65                      70                      75                      80

Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
      85                      90                      95

Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
      100                      105                      110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
      115                      120                      125

Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
      130                      135                      140

Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
      145                      150                      155                      160

Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
      165                      170                      175

Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
      180                      185                      190

Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
      195                      200                      205

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Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu  
 210 215 220  
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn  
 225 230 235 240  
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val  
 245 250 255  
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala  
 260 265 270  
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala  
 275 280 285  
 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly  
 290 295 300  
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val  
 305 310 315 320  
 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg  
 325 330 335  
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly  
 340 345 350  
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly  
 355 360 365  
 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met  
 370 375 380  
 Pro His Ser Pro Ala Ala Gly  
 385 390

<210> 27  
 <211> 447  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> TbRa12

<400> 27  
 cggtatgaac acggccgcgt ccgataactt ccagctgtcc caggggtgggc agggattcgc 60  
 cattccgatac gggcaggcga tggcgatcgc gggccagatc cgatcgggtg gggggtcacc 120  
 caccgttcac atcgggccta ccgccttcc cggcttgggt gttgtcgaca acaacggcaa 180  
 cggcgacga gtccaacgcg tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240  
 cggcgacgtg atcaccgcgg tcgacggcgc tccgatcaac tcggccaccg cgatggcgga 300  
 cgcgcttaac gggcatcatc ccggtgacgt catctcgggtg aactggcaaa ccaagtcggg 360  
 cggcacgcgt acagggaacg tgacattggc cgaggggaccc ccggcctgat ttcgtcgygg 420  
 ataccacccg ccggccggcc aattgga 447

<210> 28  
 <211> 132  
 <212> PRT  
 <213> Mycobacterium tuberculosis



<220>  
 <223> TbRa12

<400> 28  
 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe  
 1 5 10 15  
 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser  
 20 25 30  
 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly  
 35 40 45  
 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val  
 50 55 60  
 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val  
 65 70 75 80  
 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala  
 85 90 95  
 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp  
 100 105 110  
 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu  
 115 120 125  
 Gly Pro Pro Ala  
 130

<210> 29  
 <211> 1872  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> TbRa35 (Mtb32A)

<220>  
 <221> modified\_base  
 <222> (1)..(1872)  
 <223> n = g, a, c or t

<400> 29  
 gactacgttg gtgtagaaaa atcctgcccgc ccggaccctt aaggctggga caatttctga 60  
 tagctacccc gacacaggag gttacgggat gagcaattcg cgccgccgct cactcaggtg 120  
 gtcattggttg ctgagcgtgc tggctgccgt cgggctgggc ctggccacgg cgccggccca 180  
 ggcggccccc ccggccttgt cgcaggaccg gttcgccgac ttccccgcgc tgccctcga 240  
 cccgtccgcg atggtcgccc aagtggcgcc acaggtggtc aacatcaaca ccaaactggg 300  
 ctacaacaac gccgtgggcg ccgggaccgg catcgatcat gatcccaacg gtgtcgtgct 360  
 gaccaacaac cacgtgatcg cgggcgccac cgacatcaat gcgttcagcg tgggtcccg 420  
 ccaaacctac ggcgtcgatg tggctgggta tgaccgcacc caggatgtcg cgggtgctgca 480  
 gctgcgcggt gccggtggcc tgccgtcggc ggcgatcggg ggcggcgctc cgggttggtga 540  
 gcccgctcgc gcgatgggca acagcgttgg gcagggcgga acgcccctg cgggtgcctg 600  
 cagggtggtc gcgctcggcc aaaccgtgca ggcgtcggat tcgctgaccg gtgccgaaga 660  
 gacattgaac gggttgatcc agttcgatgc cgcaatccag cccggtgatt cgggcgggccc 720  
 cgctcgtcaac ggcctaggac aggtggtcgg tatgaacacg gccgcgtccg ataacttcca 780  
 gctgtcccag ggtgggcagg gattcgccat tccgatcggg caggcgatgg cgatcgccgg 840  
 ccaaattccga tcgggtgggg ggtcaccac cggtcatatc ggcctaccg ccttcctcgg 900

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cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc caacgcgtgg tcggaagcgc 960
tccggcggca agtctcggca tctccaccgg cgacgtgata accgcggtcg acggcgctcc 1020
gatcaactcg gccaccgcga tggcggacgc gcttaacggg catcatcccg gtgacgtcat 1080
ctcgggtgaac tggcaaacca agtcgggagg cagcgtatac gggaaacgtga cattggccga 1140
gggacccccg gcctgatttg tcgcggatac caccgcggcg ccggccaatt ggattggcgc 1200
cagccgtgat tgccgcgtga gccccgagt tccgtctccc gtgcgcgtgg cattgtggaa 1260
gcaatgaacg aggcagaaca cagcgttgag caccctcccc tgcagggcag ttacgtcgaa 1320
ggcgggtgtg tcgagcatcc ggatgccaag gacttcggca gcgccgccgc cctgccccgc 1380
gatccgacct ggtttaagca cgccgtcttc tacgaggtgc tggtcggggc gttcttcgac 1440
gccagcgcgg acggttccgn cgatctgcgt ggactcatcg atcgctcga ctacctgcag 1500
tggcttgcca tcgactgcat ctggtgccgc cgttcctacg actcaccgct gcgcgacggc 1560
ggttacgaca ttcgcgactt ctacaaggtg ctgcccgaat tcggcaccgt cgacgatttc 1620
gtcgccctgg tcgacaccgc tcaccggcga ggtatccgca tcatcaccga cctggtgatg 1680
aatcacacct cggagtcgca cccctgggtt caggagtccc gccgcgaccc agacggaccg 1740
tacggtgact attacgtgtg gagcgacacc agcgagcgct acaccgacgc ccggtatcatc 1800
ttcgtcgaca ccgaagagtc gaactggtca ttcgatcctg tccgccgaca gttntactg 1860
gcaccgattc tt                                     1872

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<210> 30
<211> 355
<212> PRT
<213> Mycobacterium tuberculosis

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<220>
<223> TbRa35 (Mtb32A)

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<400> 30
Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1              5              10              15

Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
      20              25              30

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
      35              40              45

Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
      50              55              60

Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
      65              70              75              80

Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
      85              90              95

Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
      100             105             110

Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
      115             120             125

Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
      130             135             140

Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
      145             150             155             160

Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
      165             170             175

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Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr  
 180 185 190  
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser  
 195 200 205  
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr  
 210 215 220  
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala  
 225 230 235 240  
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly  
 245 250 255  
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu  
 260 265 270  
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val  
 275 280 285  
 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile  
 290 295 300  
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp  
 305 310 315 320  
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln  
 325 330 335  
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly  
 340 345 350  
 Pro Pro Ala  
 355

<210> 31  
 <211> 1441  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> MTCC#2 (Mtb41)

<400> 31  
 gaggttgctg gcaatggatt tcgggctttt acctccggaa gtgaattcaa gccgaatgta 60  
 ttccggtccg gggccggagt cgatgctagc cgccgcggcc gcctgggacg gtgtggccgc 120  
 ggagttgact tccgccgcgg tctcgtagtg atcgggtggtg tcgacgctga tcgttgagcc 180  
 gtggatgggg ccggcgggcg ccgcgatggc ggccgcggca acgcccgtatg tggggtggct 240  
 ggccgccacg gcggcgctgg cgaaggagac ggccacacag gcgagggcag cggcggaagc 300  
 gtttgggacg gcgttcgcga tgacgggtgcc accatccctc gtcgcggcca accgcagccg 360  
 gttgatgtcg ctggtcgcgg cgaacattct ggggcaaaac agtgcggcga tcgcggctac 420  
 ccaggccgag tatgccgaaa tgtgggcccc agacgctgcc gtgatgtaca gctatgaggg 480  
 ggcattctcg gccgcgtcgg cgttgccgcc gttcactcca cccgtgcaag gcaccggccc 540  
 ggccggggccc gcggccgcag ccgcggcgac ccaagccgcc ggtgcgggcg ccgttgcgga 600  
 tgcacaggcg acactggccc agctgcccc ggggatcctg agcgacattc tgtccgcatt 660  
 ggccgccaac gctgatccgc tgacatcggg actgttgggg atcgcgctga ccctcaaccc 720  
 gcaagtcgga tccgctcagc cgatagtgat cccaccccc ataggggaat tggacgtgat 780  
 cgcgctctac attgcatcca tcgcgaccgg cagcattgcg ctgcgcatca cgaacacggc 840  
 cagaccctgg cacatcggcc tatacgggaa cgccggcggg ctgggaccga cgcagggcca 900

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tccactgagt tcggcgaccg acgagccgga gccgcactgg gggcccttcg ggggcgcggc 960
gccggtgtcc gcggggtcgc gccacgcagc attagtcgga gcgttgctcg tgccgcacag 1020
ctggaccacg gccgccccgg agatccagct cgccgttcag gcaacaccca ccttcagctc 1080
cagcgccggc gccgaccga cggccctaaa cgggatgccg gcaggcctgc tcagcgggat 1140
ggctttggcg agcctggccg cacgcggcac gacgggctgt ggcggcaccc gtagcggcac 1200
cagcactgac ggccaagagg acggccgcaa acccccggtg gttgtgatta gagagcagcc 1260
gccgccccga aacccccgcg ggtaaaagtc cggcaaccgt tcgtcgccgc gcggaaaatg 1320
cctggtgagc gtggctatcc gacgggcccgt tcacaccgct tgtagtagcg tacggctatg 1380
gacgacggtg tctggattct cggcggctat cagagcgatt ttgctcgcaa cctcagcaaa 1440
g
1441

```

```

<210> 32
<211> 423
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> MTTC#2 (Mtb41)

```

```

<400> 32
Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
  1             5             10             15

Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
          20             25             30

Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
          35             40             45

Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
          50             55             60

Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
          65             70             75             80

Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
          85             90             95

Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
          100            105            110

Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
          115            120            125

Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
          130            135            140

Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
          145            150            155            160

Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
          165            170            175

Ala Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
          180            185            190

Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
          195            200            205

```

Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr  
 210 215 220  
 Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser  
 225 230 235 240  
 Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile  
 245 250 255  
 Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile  
 260 265 270  
 Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly  
 275 280 285  
 Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu  
 290 295 300  
 Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala  
 305 310 315 320  
 Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser  
 325 330 335  
 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro  
 340 345 350  
 Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met  
 355 360 365  
 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg  
 370 375 380  
 Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly  
 385 390 395 400  
 Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro  
 405 410 415  
 Pro Pro Gly Asn Pro Pro Arg  
 420

<210> 33  
 <211> 1742  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb9.9A (MTI-A)

<220>  
 <221> modified\_base  
 <222> (1)..(1742)  
 <223> n = g, a, c or t

<400> 33  
 ccgctctctt tcaacgtcat aagttcgggtg ggccagtcgg ccgcgcgtgc atatggcacc 60  
 aataacgcgt gtcccatgga taccgggacc gcacgacggt agagcggatc agcgcagccg 120  
 gtgccgaaca ctaccgcgtc cacgtcagc cctgccgcgt tgcggaagat cgagcccagg 180  
 ttctcatggt cgттаacgcc ttccaacact gcgacgggtgc gcgccccggc gaccacctga 240

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gcaacgctcg gctccggcac ccggcgcgcg gctgccaaaca cccacgatt gagatggaag 300
ccgatcaccg gtgccatgac atcagccgac gctcgatagt acggcgcgcc gacaccggcc 360
agatcatcct tgagctcggc cagccggcgg tcggtgccga acagcgccag cggcgtgaac 420
cgtgaggcca gcatgcgctg caccaccagc acaccctcgg cgatcaccaa cgccttgccg 480
gtcggcagat cgggacnacn gtcgatgctg ttcaggtcac ggaaatcgtc gagccgtggg 540
tcgtcgggat cgcagacgtc ctgaacatcg aggccgtcgg ggtgctgggc acaacggcct 600
tcggtcacgg gctttcgtcg accagagcca gcatcagatc ggcgcgctg cgcaggatgt 660
cacgctcgct gcggttcagc gtcgcgagcc gctcagccag ccactcttgc agagagccgt 720
tgctgggatt aattgggaga ggaagacagc atgtcgttcg tgaccacaca gccggaagcc 780
ctggcagctg cggcgcgcaa cctacagggg attggcacga caatgaacgc ccagaacgcg 840
gcccgcgctg ctccaaccac cggagtagtg cccgcagccg ccgatgaagt atcagcgctg 900
accgcggctc agtttgctgc gcacgcgcag atgtaccaa cggtcagcgc ccaggccgcg 960
gccattcacg aaatgttcgt gaacacgctg gtggccagtt ctggctcata cgcgccacc 1020
gaggcgccca acgcagccgc tgcggctcgc acgaacctgc tgaaggagag 1080
ggggaacatc cggagttctc gggtcagggg ttgcgccagc gccagccga ttcagntatc 1140
ggcgctcata acagcagacg atctaggcat tcagtactaa ggagacaggc aacatggcct 1200
cacgttttat gacggatccg catgcgatgc gggacatggc gggccgtttt gaggtgcacg 1260
cccagacggg ggaggacgag gctcgccgga tgtgggcgtc cgcgcaaac atttccggtg 1320
cgggctggag tggcatggcc gaggcgacct cgctagacac catgacctag atgaatcagg 1380
cgtttcgcaa catcgtgaac atgctgcacg ggggtcgtga cgggctggtt cgcgacgcca 1440
acaantacga acagcaagag caggcctccc agcagatcct gagcagntag cgccgaaagc 1500
cacagctgng tacgntttct cacattagga gaacaccaat atgacgatta attaccagtt 1560
cggggacgtc gacgctcatg gcgccatgat ccgcgctcag gcggcgctcg ttgaggcgga 1620
gcatcaggcc atcgttcgtg atgtgttggc cgcgggtgac ttttggggcg gcgccggttc 1680
ggtggcttgc caggagttca ttaccaggtt gggccgtaac ttccaggtga tctacgagca 1740
gg

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<210> 34
<211> 94
<212> PRT
<213> Mycobacterium tuberculosis

```

```

<220>
<223> Mtb9.9A (MTI-A)

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```

<400> 34
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1             5             10            15

Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
      20             25             30

Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
      35             40             45

Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
      50             55             60

Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
      65             70             75            80

Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
      85             90

```

```

<210> 35
<211> 585
<212> DNA
<213> Mycobacterium tuberculosis

```

<220>  
 <223> Mtb9.8 (MSL)

<400> 35  
 tggattccga tagcgggtttc ggccctcga cgggcgacca cggcgcgag gcctccgaac 60  
 ggggggcccgg gacgctggga ttccgcccga ccgcaacaa agaacgccgg gtccgggccc 120  
 tcgggctgac cgcactggcc ggtgatgagt tcggcaacgg cccccggatg ccgatgggtgc 180  
 cggggacctg ggagcagggc agcaacgagc ccgaggcgcc cgacggatcg gggagagggg 240  
 gaggcgacgg cttaccgcac gacagcaagt aaccgaattc cgaatcacgt ggacccttac 300  
 gggtcgaaaag gagagatggt atgagccttt tggatgctca tatcccacag ttgggtggcct 360  
 cccagtcggc gtttgccgcc aaggcggggc tgatgcggca cacgatcggg caggccgagc 420  
 aggcggcgat gtcggctcag gcgtttcacc agggggagtc gtcggcgggc tttcaggccg 480  
 cccatgcccg gtttgtggcg gcggccgcc aagtcaacac cttgttgat gtcgcgagc 540  
 cgaatctggg tgaggccgcc ggtacctatg tggccgccga tgctg 585

<210> 36  
 <211> 97  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb9.8 (MSL)

<400> 36  
 Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser  
 1 5 10 15  
 Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala  
 20 25 30  
 Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser  
 35 40 45  
 Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys  
 50 55 60  
 Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala  
 65 70 75 80  
 Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly  
 85 90 95  
 Phe

<210> 37  
 <211> 500  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb8.4 (DPV)

<400> 37  
 cgtggcaatg tcgttgaccg tcggggcccgg ggtcgccctc gcagatcccg tggacgcggg 60  
 cattaacacc acctgcaatt acgggcaggt agtagctgcg ctcaacgcga cggatccggg 120  
 ggctgccgca cagttcaacg cctcaccggg ggccgagtcg tatttgcgca atttcctcgc 180  
 cgcaccgcc cctcagcgcg ctgccatggc cgcgcaattg caagctgtgc cgggggccc 240  
 acagtacatc ggccttgctg agtcggttgc cggctcctgc aacaactatt aagcccatgc 300  
 gggcccatc ccgcgaccg gcatcgctgc cggggctagg ccagattgcc ccgctcctca 360

acgggcccga tcccgcgacc cggcatcgtc gccggggcta ggccagattg ccccgctcct 420  
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<210> 38  
 <211> 96  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb8.4 (DPV)

<400> 38  
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                   20                  25                  30  
 Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser  
                   35                  40                  45  
 Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro  
           50                  55                  60  
 Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala  
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 Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr  
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<210> 39  
 <211> 999  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> DPEP

<400> 39  
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 cccgcgaccg ccaacgccga tccggagcca gcgcccccg taccacacaac ggccgcctcg 180  
 ccgcccgtcga ccgctgcagc gccaccgcga ccggcgacac ctggtgcccc cccaccaccg 240  
 gccgcccga acacgccgaa tgcccagccg ggcgatccca acgcagcacc tccgcccggc 300  
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 gacaaccggg ttggaggatt cagcttcgcg ctgcctgctg gctgggtgga gtctgacgcc 420  
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<210> 40  
 <211> 332  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> DPEP

<400> 40

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			20					25					30		
Ala	Ser	Leu	Val	Thr	Val	Ala	Val	Pro	Ala	Thr	Ala	Asn	Ala	Asp	Pro
		35					40					45			
Glu	Pro	Ala	Pro	Pro	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro	Ser	Thr
	50					55					60				
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro	Pro	Pro
65					70					75					80
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn	Ala	Ala
			85					90						95	
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Val	Ile	Ala	Pro
			100					105					110		
Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	Pro	Val	Gly	Gly	Phe	Ser
		115					120					125			
Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser	Asp	Ala	Ala	His	Phe	Asp
	130					135					140				
Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	Gly	Asp	Pro	Pro	Phe	Pro
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Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr	Arg	Ile	Val	Leu	Gly	Arg
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Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu	Ala	Thr	Asp	Ser	Lys	Ala
			180					185					190		
Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu	Phe	Tyr	Met	Pro	Tyr	Pro
		195					200					205			
Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser	Leu	Asp	Ala	Asn	Gly	Val
	210					215					220				
Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys
225					230					235					240
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn
				245					250					255	
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly
		260						265					270		

Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu  
 275 280 285

Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro  
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Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr  
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Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala  
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<210> 41

<400> 41

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<210> 42

<400> 42

000

<210> 43

<211> 339

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> DPPD

<400> 43

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 ggctattgcc cgggtggccg atgggggtttt ggcgacttgg ccgtgtgcga cggcgagaag 180  
 taccgacg gctcgttttg gcaccagtgg atgcaaactg gggttaccgg ccacagttt 240  
 tacttcgatt gtgtcagcgg cggtagcccc ctccccggcc cgccgccacc ggggtggttgc 300  
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<210> 44

<211> 112

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> DPPD

<400> 44

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala  
 1 5 10 15

Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp  
 20 25 30

Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp  
 35 40 45

Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly  
 50 55 60

Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe  
 65 70 75 80

Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro  
 85 90 95

Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro  
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<210> 45

<211> 154

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> ESAT-6

<400> 45

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 aatgtcacgt ccattcattc cctccttgac gaggggaagc agtccctgac caagctcgca 120  
 gcggcctggg gcggtagcgg ttcggaagcg tacc 154

<210> 46

<211> 51

<212> PRT

<213> Mycobacterium tuberculosis

<220>

<223> ESAT-6

<400> 46

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser  
 1 5 10 15

Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly  
 20 25 30

Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser  
 35 40 45

Glu Ala Tyr  
 50

<210> 47

<211> 2310

<212> DNA

<213> Mycobacterium tuberculosis

<220>

<223> Mtb82

<400> 47

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 aacgttcggg ccccgccacc caaccggcgg acgcccagac cgcgacgtcc gcgacgggtc 120  
 gacccttgag caccagggcg gtgttcgcc ccgatttcgg cgatgaggac aacttcccc 180

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atccgacgct cggcccgag accgagccgc aagaccggat ggccaccacc agccgggtgc 240
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gtccctattg cggcagcccg tattcgttcc tgccgcagct aaatcccggg gacatcgctc 480
ccggccagta cgaggtcaaa ggctgcatcg cgacggcgcg actgggctgg atctacctcg 540
ctctcgaccg caatgtcaac ggccgtccgg tgggtgtcaa gggcctgggt cattccggtg 600
atgccgaagc gcaggcaatg gcgatggccg aacgccagtt cctggccgag gtggtgcacc 660
cgtcgatcgt gcagatcttc aactttgtcg agcacaccga caggcacggg gatccggtcg 720
gctacatcgt gatggaatac gtcggcgggc aatcgctcaa acgcagcaag ggtcagaaac 780
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gcgcgctgga ctggctgaag gacaacaagg ccagcaccaa ccacatcctc gggttcccgt 2160
tcaccagtca cgggctgcgg ctgggtgtcg aggcgtcact gcgcagcctg gcccgggtag 2220
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gcacgttcta agccgccga gtgtgaatcg 2310

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<210> 48  
 <211> 750  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb82

<400> 48  
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 35 40 45  
 Pro Thr Leu Gly Pro Asp Thr Glu Pro Gln Asp Arg Met Ala Thr Thr  
 50 55 60  
 Ser Arg Val Arg Pro Pro Val Arg Arg Leu Gly Gly Gly Leu Val Glu  
 65 70 75 80

Ile Pro Arg Ala Pro Asp Ile Asp Pro Leu Glu Ala Leu Met Thr Asn  
                                     85                                    90                                    95  
 Pro Val Val Pro Glu Ser Lys Arg Phe Cys Trp Asn Cys Gly Arg Pro  
                                     100                                    105                                    110  
 Val Gly Arg Ser Asp Ser Glu Thr Lys Gly Ala Ser Glu Gly Trp Cys  
                                     115                                    120                                    125  
 Pro Tyr Cys Gly Ser Pro Tyr Ser Phe Leu Pro Gln Leu Asn Pro Gly  
                                     130                                    135                                    140  
 Asp Ile Val Ala Gly Gln Tyr Glu Val Lys Gly Cys Ile Ala His Gly  
 145                                    150                                    155                                    160  
 Gly Leu Gly Trp Ile Tyr Leu Ala Leu Asp Arg Asn Val Asn Gly Arg  
                                     165                                    170                                    175  
 Pro Val Val Leu Lys Gly Leu Val His Ser Gly Asp Ala Glu Ala Gln  
                                     180                                    185                                    190  
 Ala Met Ala Met Ala Glu Arg Gln Phe Leu Ala Glu Val Val His Pro  
                                     195                                    200                                    205  
 Ser Ile Val Gln Ile Phe Asn Phe Val Glu His Thr Asp Arg His Gly  
                                     210                                    215                                    220  
 Asp Pro Val Gly Tyr Ile Val Met Glu Tyr Val Gly Gly Gln Ser Leu  
 225                                    230                                    235                                    240  
 Lys Arg Ser Lys Gly Gln Lys Leu Pro Val Ala Glu Ala Ile Ala Tyr  
                                     245                                    250                                    255  
 Leu Leu Glu Ile Leu Pro Ala Leu Ser Tyr Leu His Ser Ile Gly Leu  
                                     260                                    265                                    270  
 Val Tyr Asn Asp Leu Lys Pro Glu Asn Ile Met Leu Thr Glu Glu Gln  
                                     275                                    280                                    285  
 Leu Lys Leu Ile Asp Leu Gly Ala Val Ser Arg Ile Asn Ser Phe Gly  
                                     290                                    295                                    300  
 Tyr Leu Tyr Gly Thr Pro Gly Phe Gln Ala Pro Glu Ile Val Arg Thr  
 305                                    310                                    315                                    320  
 Gly Pro Thr Val Ala Thr Asp Ile Tyr Thr Val Gly Arg Thr Leu Ala  
                                     325                                    330                                    335  
 Ala Leu Thr Leu Asp Leu Pro Thr Arg Asn Gly Arg Tyr Val Asp Gly  
                                     340                                    345                                    350  
 Leu Pro Glu Asp Asp Pro Val Leu Lys Thr Tyr Asp Ser Tyr Gly Arg  
                                     355                                    360                                    365  
 Leu Leu Arg Arg Ala Ile Asp Pro Asp Pro Arg Gln Arg Phe Thr Thr  
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 Ala Glu Glu Met Ser Ala Gln Leu Thr Gly Val Leu Arg Glu Val Val  
 385                                    390                                    395                                    400

Ala Gln Asp Thr Gly Val Pro Arg Pro Gly Leu Ser Thr Ile Phe Ser  
 405 410 415  
 Pro Ser Arg Ser Thr Phe Gly Val Asp Leu Leu Val Ala His Thr Asp  
 420 425 430  
 Val Tyr Leu Asp Gly Gln Val His Ala Glu Lys Leu Thr Ala Asn Glu  
 435 440 445  
 Ile Val Thr Ala Leu Ser Val Pro Leu Val Asp Pro Thr Asp Val Ala  
 450 455 460  
 Ala Ser Val Leu Gln Ala Thr Val Leu Ser Gln Pro Val Gln Thr Leu  
 465 470 475 480  
 Asp Ser Leu Arg Ala Ala Arg His Gly Ala Leu Asp Ala Asp Gly Val  
 485 490 495  
 Asp Phe Ser Glu Ser Val Glu Leu Pro Leu Met Glu Val Arg Ala Leu  
 500 505 510  
 Leu Asp Leu Gly Asp Val Ala Lys Ala Thr Arg Lys Leu Asp Asp Leu  
 515 520 525  
 Ala Glu Arg Val Gly Trp Arg Trp Arg Leu Val Trp Tyr Arg Ala Val  
 530 535 540  
 Ala Glu Leu Leu Thr Gly Asp Tyr Asp Ser Ala Thr Lys His Phe Thr  
 545 550 555 560  
 Glu Val Leu Asp Thr Phe Pro Gly Glu Leu Ala Pro Lys Leu Ala Leu  
 565 570 575  
 Ala Ala Thr Ala Glu Leu Ala Gly Asn Thr Asp Glu His Lys Phe Tyr  
 580 585 590  
 Gln Thr Val Trp Ser Thr Asn Asp Gly Val Ile Ser Ala Ala Phe Gly  
 595 600 605  
 Leu Ala Arg Ala Arg Ser Ala Glu Gly Asp Arg Val Gly Ala Val Arg  
 610 615 620  
 Thr Leu Asp Glu Val Pro Pro Thr Ser Arg His Phe Thr Thr Ala Arg  
 625 630 635 640  
 Leu Thr Ser Ala Val Thr Leu Leu Ser Gly Arg Ser Thr Ser Glu Val  
 645 650 655  
 Thr Glu Glu Gln Ile Arg Asp Ala Ala Arg Arg Val Glu Ala Leu Pro  
 660 665 670  
 Pro Thr Glu Pro Arg Val Leu Gln Ile Arg Ala Leu Val Leu Gly Gly  
 675 680 685  
 Ala Leu Asp Trp Leu Lys Asp Asn Lys Ala Ser Thr Asn His Ile Leu  
 690 695 700  
 Gly Phe Pro Phe Thr Ser His Gly Leu Arg Leu Gly Val Glu Ala Ser  
 705 710 715 720

Leu Arg Ser Leu Ala Arg Val Ala Pro Thr Gln Arg His Arg Tyr Thr  
725 730 735

Leu Val Asp Met Ala Asn Lys Val Arg Pro Thr Ser Thr Phe  
740 745 750

<210> 49  
<211> 1920  
<212> DNA  
<213> Mycobacterium tuberculosis

<220>  
<223> Mtb59

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ctctttcacc gccgacacca gtagagagga agtcggtagc gtcgtcgatg ccggggacgg 180  
catcgacac gtcgagggtt tgccatcggt gatgaccaa gagctgctcg aattcccggg 240  
cggaatcctc ggcgtcgccc tcaacctcga cgagcacagc gtcggcgagg tgatcctcgg 300  
tgacttcgag aacatcgaag aaggctcagc ggtaaccgc accggcgaag tcttatcggg 360  
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gcgcggagac gtcgactccg atactcggcg cgcgctggag ctccaggcgc cctcgggtgg 480  
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cccgatcggc cgcggccagc gccagctgat catcgcgac cgcaagaccg gcaaaaccgc 600  
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gcagggtgcgc tgtgtatacg tggccatcgg gcagaaggga actaccatcg ccgcggtagc 720  
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agagattttg actgagatcc gggacagcca aaagctcacc gaggaggcgc ccgacaagct 1560  
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tgcgacatcg cgcacgcca gggcgaggc tcggctcgag tccgctcggc cctacgcttt 1860  
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<210> 50  
<211> 549  
<212> PRT  
<213> Mycobacterium tuberculosis

<220>  
<223> Mtb59

<400> 50  
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 Thr Val Val Asp Ala Gly Asp Gly Ile Ala His Val Glu Gly Leu Pro  
                   35                  40                  45  
 Ser Val Met Thr Gln Glu Leu Leu Glu Phe Pro Gly Gly Ile Leu Gly  
                   50                  55                  60  
 Val Ala Leu Asn Leu Asp Glu His Ser Val Gly Ala Val Ile Leu Gly  
                   65                  70                  75                  80  
 Asp Phe Glu Asn Ile Glu Glu Gly Gln Gln Val Lys Arg Thr Gly Glu  
                   85                  90                  95  
 Val Leu Ser Val Pro Val Gly Asp Gly Phe Leu Gly Arg Val Val Asn  
                   100                  105                  110  
 Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr  
                   115                  120                  125  
 Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val His Arg Gln Gly  
                   130                  135                  140  
 Val Lys Glu Pro Leu Gln Thr Gly Ile Lys Ala Ile Asp Ala Met Thr  
                   145                  150                  155                  160  
 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr  
                   165                  170                  175  
 Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Arg Gln Asn  
                   180                  185                  190  
 Trp Glu Ser Gly Asp Pro Lys Lys Gln Val Arg Cys Val Tyr Val Ala  
                   195                  200                  205  
 Ile Gly Gln Lys Gly Thr Thr Ile Ala Ala Val Arg Arg Thr Leu Glu  
                   210                  215                  220  
 Glu Gly Gly Ala Met Asp Tyr Thr Thr Ile Val Ala Ala Ala Ala Ser  
                   225                  230                  235                  240  
 Glu Ser Ala Gly Phe Lys Trp Leu Ala Pro Tyr Thr Gly Ser Ala Ile  
                   245                  250                  255  
 Ala Gln His Trp Met Tyr Glu Gly Lys His Val Leu Ile Ile Phe Asp  
                   260                  265                  270  
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu  
                   275                  280                  285  
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu  
                   290                  295                  300  
 His Ser Arg Leu Leu Glu Arg Cys Ala Lys Leu Ser Asp Asp Leu Gly  
                   305                  310                  315                  320  
 Gly Gly Ser Leu Thr Gly Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp  
                   325                  330                  335



Ile Ser Ala Tyr Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln  
 340 345 350  
 Cys Phe Leu Glu Thr Asp Leu Phe Asn Gln Gly Val Arg Pro Ala Ile  
 355 360 365  
 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Ile Lys  
 370 375 380  
 Ala Met Lys Glu Val Ala Gly Ser Leu Arg Leu Asp Leu Ser Gln Tyr  
 385 390 395 400  
 Arg Glu Leu Glu Ala Phe Ala Ala Phe Ala Ser Asp Leu Asp Ala Ala  
 405 410 415  
 Ser Lys Ala Gln Leu Glu Arg Gly Ala Arg Leu Val Glu Leu Leu Lys  
 420 425 430  
 Gln Pro Gln Ser Gln Pro Met Pro Val Glu Glu Gln Val Val Ser Ile  
 435 440 445  
 Phe Leu Gly Thr Gly Gly His Leu Asp Ser Val Pro Val Glu Asp Val  
 450 455 460  
 Arg Arg Phe Glu Thr Glu Leu Leu Asp His Met Arg Ala Ser Glu Glu  
 465 470 475 480  
 Glu Ile Leu Thr Glu Ile Arg Asp Ser Gln Lys Leu Thr Glu Glu Ala  
 485 490 495  
 Ala Asp Lys Leu Thr Glu Val Ile Lys Asn Phe Lys Lys Gly Phe Ala  
 500 505 510  
 Ala Thr Gly Gly Gly Ser Val Val Pro Asp Glu His Val Glu Ala Leu  
 515 520 525  
 Asp Glu Asp Lys Leu Ala Lys Glu Ala Val Lys Val Lys Lys Pro Ala  
 530 535 540  
 Pro Lys Lys Lys Lys  
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<210> 51

<211> 3523

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TbF14 fusion protein

<400> 51

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 agcttctggg cgggcgtcga caaggtcgtc gccgacctga cccgcagaa ccaagctctg 180  
 ttgaacgccc gcgacgagct gcaggcgcag atcgacaagt ggcaccggcg tcgggtgatc 240  
 gagcccatcg acatggatgc ctaccgccag ttcctcaccg agatcggcta cctgcttccc 300  
 gaacctgatg acttcacat caccacgtcc ggtgtcgacg ctgagatcac cagaccgcc 360  
 ggccccagc tgggtggtgcc ggtgtcgaac gcgcggtttg ctctgaacgc ggccaacgct 420  
 cgctggggct ccctctacga cgccttgtat ggcaccgatg tcatccccga gaccgacggc 480

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acagtgcagg atggccagct cgtgggttgc ttgccggata agtccaccgg cctggccaac 660
cccggccagt tcgcccgtta caccggcgca gccgagtcgc cgacatcggg gctgctaata 720
aatcacgggt tgcacatcga gatcctgata gatccggagt cgcaggtcgg caccaccgac 780
cgggcccggc tcaaggacgt gatectggaa tccgcgatca ccacgatcat ggacttcgag 840
gactcgggtg ccgcccgtga cgccgccgac aaggtgctgg gttatcgga ctggctcggc 900
ctgaacaagg gcgacctggc agcagcggta gacaaggacg gcaccgcttt cctgcccgtg 960
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gacggcagcg aggtgttcga aggcacatg gatgcccctat tcaccggcct gatcgccatc 1140
cacgggctaa aggccagcga cgtcaacggg ccgctgatca acagccgcac cggctccatc 1200
tacatcgtca agccgaagt gcacgggtcg gccgaggtgg cgtttacctg cgaactgttc 1260
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gaccacaacg tcgatgccgg cctggccgcc ggggttcagc gccgagccca ggtcggcaag 1560
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cgggccacgc tgcgaatctc cagccaattg ttggccaact ggctgcgcca cgggtgtgatc 1980
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acaaggccgt ggtcgcgctg catgaagcgt tcgggctcgg cggcgacgag gaggccacgg 3480
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<210> 52
<211> 1172
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:TbF14 fusion
      protein

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<400> 52

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Pro Gly Thr Asp Ile Asp Pro Asp Ser Phe Trp Ala Gly Val Asp Lys  
35 40 45  
Val Val Ala Asp Leu Thr Pro Gln Asn Gln Ala Leu Leu Asn Ala Arg  
50 55 60  
Asp Glu Leu Gln Ala Gln Ile Asp Lys Trp His Arg Arg Arg Val Ile  
65 70 75 80  
Glu Pro Ile Asp Met Asp Ala Tyr Arg Gln Phe Leu Thr Glu Ile Gly  
85 90 95  
Tyr Leu Leu Pro Glu Pro Asp Asp Phe Thr Ile Thr Thr Ser Gly Val  
100 105 110  
Asp Ala Glu Ile Thr Thr Thr Ala Gly Pro Gln Leu Val Val Pro Val  
115 120 125  
Leu Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser  
130 135 140  
Leu Tyr Asp Ala Leu Tyr Gly Thr Asp Val Ile Pro Glu Thr Asp Gly  
145 150 155 160  
Ala Glu Lys Gly Pro Thr Tyr Asn Lys Val Arg Gly Asp Lys Val Ile  
165 170 175  
Ala Tyr Ala Arg Lys Phe Leu Asp Asp Ser Val Pro Leu Ser Ser Gly  
180 185 190  
Ser Phe Gly Asp Ala Thr Gly Phe Thr Val Gln Asp Gly Gln Leu Val  
195 200 205  
Val Ala Leu Pro Asp Lys Ser Thr Gly Leu Ala Asn Pro Gly Gln Phe  
210 215 220  
Ala Gly Tyr Thr Gly Ala Ala Glu Ser Pro Thr Ser Val Leu Leu Ile  
225 230 235 240  
Asn His Gly Leu His Ile Glu Ile Leu Ile Asp Pro Glu Ser Gln Val  
245 250 255  
Gly Thr Thr Asp Arg Ala Gly Val Lys Asp Val Ile Leu Glu Ser Ala  
260 265 270  
Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala  
275 280 285  
Ala Asp Lys Val Leu Gly Tyr Arg Asn Trp Leu Gly Leu Asn Lys Gly  
290 295 300  
Asp Leu Ala Ala Ala Val Asp Lys Asp Gly Thr Ala Phe Leu Arg Val  
305 310 315 320

Leu Asn Arg Asp Arg Asn Tyr Thr Ala Pro Gly Gly Gly Gln Phe Thr  
 325 330 335  
 Leu Pro Gly Arg Ser Leu Met Phe Val Arg Asn Val Gly His Leu Met  
 340 345 350  
 Thr Asn Asp Ala Ile Val Asp Thr Asp Gly Ser Glu Val Phe Glu Gly  
 355 360 365  
 Ile Met Asp Ala Leu Phe Thr Gly Leu Ile Ala Ile His Gly Leu Lys  
 370 375 380  
 Ala Ser Asp Val Asn Gly Pro Leu Ile Asn Ser Arg Thr Gly Ser Ile  
 385 390 395 400  
 Tyr Ile Val Lys Pro Lys Met His Gly Pro Ala Glu Val Ala Phe Thr  
 405 410 415  
 Cys Glu Leu Phe Ser Arg Val Glu Asp Val Leu Gly Leu Pro Gln Asn  
 420 425 430  
 Thr Met Lys Ile Gly Ile Met Asp Glu Glu Arg Arg Thr Thr Val Asn  
 435 440 445  
 Leu Lys Ala Cys Ile Lys Ala Ala Ala Asp Arg Val Val Phe Ile Asn  
 450 455 460  
 Thr Gly Phe Leu Asp Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu  
 465 470 475 480  
 Ala Gly Pro Met Val Arg Lys Gly Thr Met Lys Ser Gln Pro Trp Ile  
 485 490 495  
 Leu Ala Tyr Glu Asp His Asn Val Asp Ala Gly Leu Ala Ala Gly Phe  
 500 505 510  
 Ser Gly Arg Ala Gln Val Gly Lys Gly Met Trp Thr Met Thr Glu Leu  
 515 520 525  
 Met Ala Asp Met Val Glu Thr Lys Ile Ala Gln Pro Arg Ala Gly Ala  
 530 535 540  
 Ser Thr Ala Trp Val Pro Ser Pro Thr Ala Ala Thr Leu His Ala Leu  
 545 550 555 560  
 His Tyr His Gln Val Asp Val Ala Ala Val Gln Gln Gly Leu Ala Gly  
 565 570 575  
 Lys Arg Arg Ala Thr Ile Glu Gln Leu Leu Thr Ile Pro Leu Ala Lys  
 580 585 590  
 Glu Leu Ala Trp Ala Pro Asp Glu Ile Arg Glu Glu Val Asp Asn Asn  
 595 600 605  
 Cys Gln Ser Ile Leu Gly Tyr Val Val Arg Trp Val Asp Gln Gly Val  
 610 615 620  
 Gly Cys Ser Lys Val Pro Asp Ile His Asp Val Ala Leu Met Glu Asp  
 625 630 635 640

Arg Ala Thr Leu Arg Ile Ser Ser Gln Leu Leu Ala Asn Trp Leu Arg  
 645 650 655  
 His Gly Val Ile Thr Ser Ala Asp Val Arg Ala Ser Leu Glu Arg Met  
 660 665 670  
 Ala Pro Leu Val Asp Arg Gln Asn Ala Gly Asp Val Ala Tyr Arg Pro  
 675 680 685  
 Met Ala Pro Asn Phe Asp Asp Ser Ile Ala Phe Leu Ala Ala Gln Glu  
 690 695 700  
 Leu Ile Leu Ser Gly Ala Gln Gln Pro Asn Gly Tyr Thr Glu Pro Ile  
 705 710 715 720  
 Leu His Arg Arg Arg Arg Glu Phe Lys Ala Arg Ala Ala Glu Lys Pro  
 725 730 735  
 Ala Pro Ser Asp Arg Ala Gly Asp Asp Ala Ala Arg Val Gln Lys Tyr  
 740 745 750  
 Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg Val Ala Glu  
 755 760 765  
 Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val Val Val Val  
 770 775 780  
 Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu Ala Gln Gln  
 785 790 795 800  
 Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu Leu Thr Ala  
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 Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile Glu Ser Leu  
 820 825 830  
 Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly Val Ile Thr  
 835 840 845  
 Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr Pro Gly Arg  
 850 855 860  
 Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val Ala Gly Phe  
 865 870 875 880  
 Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu Gly Arg Gly  
 885 890 895  
 Gly Ser Asp Thr Thr Ala Val Ala Met Ala Ala Ala Leu Gly Ala Asp  
 900 905 910  
 Val Cys Glu Ile Tyr Thr Asp Val Asp Gly Ile Phe Ser Ala Asp Pro  
 915 920 925  
 Arg Ile Val Arg Asn Ala Arg Lys Leu Asp Thr Val Thr Phe Glu Glu  
 930 935 940  
 Met Leu Glu Met Ala Ala Cys Gly Ala Lys Val Leu Met Leu Arg Cys  
 945 950 955 960



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<210> 54

<211> 983

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:TbF15 fusion protein

<400> 54

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Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
      20                      25                      30

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 Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val  
 50 55 60  
 Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Cys Gly Ser Lys Pro Pro  
 65 70 75 80  
 Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr  
 85 90 95  
 Pro Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu  
 100 105 110  
 Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro  
 115 120 125  
 Asn Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala  
 130 135 140  
 Gln Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu  
 145 150 155 160  
 Ser Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu  
 165 170 175  
 Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu  
 180 185 190  
 His Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr  
 195 200 205  
 Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val  
 210 215 220  
 Asn Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser  
 225 230 235 240  
 Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu  
 245 250 255  
 Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala  
 260 265 270  
 Val Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly  
 275 280 285  
 Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu  
 290 295 300  
 Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser  
 305 310 315 320  
 Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala  
 325 330 335  
 Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile  
 340 345 350



Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala  
 355 360 365  
 Ile Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln  
 370 375 380  
 Ala Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu  
 385 390 395 400  
 Asp Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser  
 405 410 415  
 Asp Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala  
 420 425 430  
 Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp  
 435 440 445  
 Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln  
 450 455 460  
 Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val  
 465 470 475 480  
 Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile  
 485 490 495  
 Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu  
 500 505 510  
 Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Thr Gln Ser Gln  
 515 520 525  
 Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn Arg Ala Asn Glu Val  
 530 535 540  
 Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val Pro Ile Thr Pro Cys  
 545 550 555 560  
 Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln Leu Val Leu Ser Ala  
 565 570 575  
 Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala Lys Glu Arg Gln Arg  
 580 585 590  
 Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala Tyr Gly Glu Val Asp  
 595 600 605  
 Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly Glu Gly Thr Val Gln  
 610 615 620  
 Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser Ser Ala Glu Leu Thr  
 625 630 635 640  
 Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro Asn Phe Met Asp Leu  
 645 650 655  
 Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp Gln Gly Ala Ser Leu  
 660 665 670

Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn Leu Thr Leu Gln Gly  
 675 680 685  
 Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp Glu Gly Asp Ala Ala  
 690 695 700  
 Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg Gln Trp Ile Leu His  
 705 710 715 720  
 Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln Ala Gln Tyr Val Ala  
 725 730 735  
 Gln Leu His Val Trp Ala Arg Arg Glu His Pro Thr Tyr Glu Asp Ile  
 740 745 750  
 Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro Ser Ala Arg Asp Gln  
 755 760 765  
 Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg Ser Glu Lys Val Leu  
 770 775 780  
 Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro Val Asn Pro Pro Lys  
 785 790 795 800  
 Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro Pro Gln Glu Gln  
 805 810 815  
 Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser Asp Gly Ser Gly Val  
 820 825 830  
 Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met Val Pro Pro Thr Gly  
 835 840 845  
 Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala Ala Gln Leu Thr Ser  
 850 855 860  
 Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp Val Ala Val Lys Ala  
 865 870 875 880  
 Ala Ser Leu Gly Gly Gly Gly Gly Gly Gly Val Pro Ser Ala Pro Leu  
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 Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg Pro Ala Gly Ala Gly  
 900 905 910  
 Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly Gly Gly Ala Ala Leu  
 915 920 925  
 Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala Ala His Gln Gly Gln  
 930 935 940  
 Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu Asp Glu Ala Leu Tyr  
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 Gln Asp Ser Lys Glu Ser Lys  
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<210> 55

<400> 55

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<210> 56

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<210> 57

<211> 2232

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein  
HTCC#1(184-392)-TbH9-HTCC#1(1-129)

<220>

<221> CDS

<222> (4)..(2226)

<400> 57

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Thr Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu	
20 25 30	
aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct	144
Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser	
35 40 45	
cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg	192
Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu	
50 55 60	
acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg	240
Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala	
65 70 75	
gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg	288
Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala	
80 85 90 95	
agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt	336
Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly	
100 105 110	
ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg	384
Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg	
115 120 125	

cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag	432
Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu	
130 135 140	
cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt	480
Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly	
145 150 155	
atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg	528
Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala	
160 165 170 175	
tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc	576
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly	
180 185 190	
act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg	624
Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly	
195 200 205	
caa aag gtg ctg gta cga aac gtc gtc gaa ttc atg gtg gat ttc ggg	672
Gln Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly	
210 215 220	
gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt	720
Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly	
225 230 235	
tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt	768
Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser	
240 245 250 255	
gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg	816
Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu	
260 265 270	
acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg	864
Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala	
275 280 285	
gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag	912
Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu	
290 295 300	
ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg	960
Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala	
305 310 315	
tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa	1008
Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu	
320 325 330 335	
ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg	1056
Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala	
340 345 350	
atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc	1104
Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala	
355 360 365	

gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg	1152
Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr	
370 375 380	
ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc	1200
Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu	
385 390 395	
ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg	1248
Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala	
400 405 410 415	
aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag	1296
Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln	
420 425 430	
ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag	1344
Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys	
435 440 445	
acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc	1392
Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala	
450 455 460	
aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc	1440
Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr	
465 470 475	
ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc	1488
Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala	
480 485 490 495	
gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc	1536
Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly	
500 505 510	
agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg	1584
Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu	
515 520 525	
ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc	1632
Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala	
530 535 540	
gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc	1680
Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr	
545 550 555	
agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg	1728
Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly	
560 565 570 575	
ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt	1776
Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly	
580 585 590	
gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca	1824
Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala	
595 600 605	

gcc ggc gat atc atg agc aga gcg ttc atc atc gat cca acg atc agt 1872  
Ala Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser  
610 615 620

gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa 1920  
Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln  
625 630 635

ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag 1968  
Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu  
640 645 650 655

gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg 2016  
Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala  
660 665 670

gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa 2064  
Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu  
675 680 685

ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc 2112  
Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala  
690 695 700

aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt 2160  
Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly  
705 710 715

ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc 2208  
Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val  
720 725 730 735

gtc ggg cac gcc cta taa gatatc 2232  
Val Gly His Ala Leu  
740

<210> 58  
<211> 740  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:fusion protein  
HTCC#1(184-392)-TbH9-HTCC#1(1-129)

<400> 58  
Met His His His His His His Asp Val Ala Asp Ile Ile Lys Gly Thr  
1 5 10 15  
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys  
20 25 30  
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg  
35 40 45  
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr  
50 55 60  
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala  
65 70 75 80



Glu Gln Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn  
 405 410 415  
 Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro  
 420 425 430  
 Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr  
 435 440 445  
 Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn  
 450 455 460  
 Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu  
 465 470 475 480  
 Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val  
 485 490 495  
 Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser  
 500 505 510  
 Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly  
 515 520 525  
 Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala  
 530 535 540  
 Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser  
 545 550 555 560  
 Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu  
 565 570 575  
 Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val  
 580 585 590  
 Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala  
 595 600 605  
 Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala  
 610 615 620  
 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly  
 625 630 635 640  
 Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu  
 645 650 655  
 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp  
 660 665 670  
 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu  
 675 680 685  
 Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn  
 690 695 700  
 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu  
 705 710 715 720



Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val  
725 730 735

Gly His Ala Leu  
740

<210> 59  
<211> 2365  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:fusion protein  
HTCC#1(1-149)-TbH9-HTCC#1(161-392)

<220>  
<221> CDS  
<222> (4) .. (2355)

<400> 59  
cat atg cat cac cat cac cat cac atg agc aga gcg ttc atc atc gat 48  
Met His His His His His His Met Ser Arg Ala Phe Ile Ile Asp  
1 5 10 15  
cca acg atc agt gcc att gac ggc ttg tac gac ctt ctg ggg att gga 96  
Pro Thr Ile Ser Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly  
20 25 30  
ata ccc aac caa ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa 144  
Ile Pro Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu  
35 40 45  
aaa gcc ctg gag gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta 192  
Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu  
50 55 60  
ggt tcg gcc gcg gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat 240  
Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn  
65 70 75  
ttt ttc cag gaa ctg gca gac ctc gat cgt cag ctc atc agc ctg atc 288  
Phe Phe Gln Glu Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile  
80 85 90 95  
cac gac cag gcc aac gcg gtc cag acg acc cgc gac atc ctg gag ggc 336  
His Asp Gln Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly  
100 105 110  
gcc aag aaa ggt ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc 384  
Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr  
115 120 125  
tac atc ccg gtc gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg 432  
Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro  
130 135 140  
ttt tgc gcg ggc gcg atg gcc gta gtg ggc ggc gcg ctt aag ctt atg 480  
Phe Cys Ala Gly Ala Met Ala Val Val Gly Gly Ala Leu Lys Leu Met  
145 150 155

gtg gat ttc ggg gcg tta cca ccg gag atc aac tcc gcg agg atg tac	528
Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr	
160 165 170 175	
gcc ggc ccg ggt tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac	576
Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp	
180 185 190	
agc gtg gcg agt gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg	624
Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val	
195 200 205	
gtc tgg ggt ctg acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg	672
Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu	
210 215 220	
atg gtg gcg gcg gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg	720
Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala	
225 230 235	
ggg cag gcc gag ctg acc gcc gcc cag gtc ccg gtt gct gcg gcg gcc	768
Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala	
240 245 250 255	
tac gag acg gcg tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag	816
Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu	
260 265 270	
aac cgt gct gaa ctg atg att ctg ata gcg acc aac ctc ttg ggg caa	864
Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln	
275 280 285	
aac acc ccg gcg atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg	912
Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp	
290 295 300	
gcc caa gac gcc gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg	960
Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr	
305 310 315	
gcg acg gcg acg ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc	1008
Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser	
320 325 330 335	
gcg ggt ggg ctc ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac	1056
Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp	
340 345 350	
acc gcc gcg gcg aac cag ttg atg aac aat gtg ccc cag gcg ctg caa	1104
Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln	
355 360 365	
cag ctg gcc cag ccc acg cag ggc acc acg cct tct tcc aag ctg ggt	1152
Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly	
370 375 380	
ggc ctg tgg aag acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg	1200
Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met	
385 390 395	

gtg	tcg	atg	gcc	aac	aac	cac	atg	tcg	atg	acc	aac	tcg	ggt	gtg	tcg	1248
Val	Ser	Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	
400					405					410					415	
atg	acc	aac	acc	ttg	agc	tcg	atg	ttg	aag	ggc	ttt	gct	ccg	gcg	gcg	1296
Met	Thr	Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	
				420					425						430	
gcc	gcc	cag	gcc	gtg	caa	acc	gcg	gcg	caa	aac	ggg	gtc	ccg	gcg	atg	1344
Ala	Ala	Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	
			435					440					445			
agc	tcg	ctg	ggc	agc	tcg	ctg	ggt	tct	tcg	ggt	ctg	ggc	ggt	ggg	gtg	1392
Ser	Ser	Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	
		450					455					460				
gcc	gcc	aac	ttg	ggt	cgg	gcg	gcc	tcg	gtc	ggt	tcg	ttg	tcg	gtg	ccg	1440
Ala	Ala	Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	
		465				470					475					
cag	gcc	tgg	gcc	gcg	gcc	aac	cag	gca	gtc	acc	ccg	gcg	gcg	cgg	gcg	1488
Gln	Ala	Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	
480					485					490					495	
ctg	ccg	ctg	acc	agc	ctg	acc	agc	gcc	gcg	gaa	aga	ggg	ccc	ggg	cag	1536
Leu	Pro	Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	
				500					505						510	
atg	ctg	ggc	ggg	ctg	ccg	gtg	ggg	cag	atg	ggc	gcc	agg	gcc	ggt	ggt	1584
Met	Leu	Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	
			515				520						525			
ggg	ctc	agt	ggt	gtg	ctg	cgt	gtt	ccg	ccg	cga	ccc	tat	gtg	atg	ccg	1632
Gly	Leu	Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	
		530					535					540				
cat	tct	ccg	gca	gcc	ggc	aag	ctt	act	caa	ctc	ctc	aaa	ttg	ctt	gcc	1680
His	Ser	Pro	Ala	Ala	Gly	Lys	Leu	Thr	Gln	Leu	Leu	Lys	Leu	Leu	Ala	
		545				550					555					
aaa	ttg	gcg	gag	ttg	gtc	gcg	gcc	gcc	att	gcg	gac	atc	att	tcg	gat	1728
Lys	Leu	Ala	Glu	Leu	Val	Ala	Ala	Ala	Ile	Ala	Asp	Ile	Ile	Ser	Asp	
560					565				570						575	
gtg	gcg	gac	atc	atc	aag	ggc	atc	ctc	gga	gaa	gtg	tgg	gag	ttc	atc	1776
Val	Ala	Asp	Ile	Ile	Lys	Gly	Ile	Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	
				580					585						590	
aca	aac	gcg	ctc	aac	ggc	ctg	aaa	gag	ctt	tgg	gac	aag	ctc	acg	ggg	1824
Thr	Asn	Ala	Leu	Asn	Gly	Leu	Lys	Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	
			595					600					605			
tgg	gtg	acc	gga	ctg	ttc	tct	cga	ggg	tgg	tcg	aac	ctg	gag	tcc	ttc	1872
Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg	Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	
		610					615					620				
ttt	gcg	ggc	gtc	ccc	ggc	ttg	acc	ggc	gcg	acc	agc	ggc	ttg	tcg	caa	1920
Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr	Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	
		625				630					635					

gtg act ggc ttg ttc ggt gcg gcc ggt ctg tcc gca tcg tcg ggc ttg	1968
Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu	
640 645 650 655	
gct cac gcg gat agc ctg gcg agc tca gcc agc ttg ccc gcc ctg gcc	2016
Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala	
660 665 670	
ggc att ggg ggc ggg tcc ggt ttt ggg ggc ttg ccg agc ctg gct cag	2064
Gly Ile Gly Gly Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln	
675 680 685	
gtc cat gcc gcc tca act cgg cag gcg cta cgg ccc cga gct gat ggc	2112
Val His Ala Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly	
690 695 700	
ccg gtc ggc gcc gct gcc gag cag gtc ggc ggg cag tcg cag ctg gtc	2160
Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val	
705 710 715	
tcc gcg cag ggt tcc caa ggt atg ggc gga ccc gta ggc atg ggc ggc	2208
Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly	
720 725 730 735	
atg cac ccc tct tcg ggg gcg tcg aaa ggg acg acg acg aag aag tac	2256
Met His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr	
740 745 750	
tcg gaa ggc gcg gcg gcg ggc act gaa gac gcc gag cgc gcg cca gtc	2304
Ser Glu Gly Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val	
755 760 765	
gaa gct gac gcg ggc ggt ggg caa aag gtg ctg gta cga aac gtc gtc	2352
Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val	
770 775 780	
taa cggcgaattc	2365

<210> 60

<211> 783

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein  
HTCC#1(1-149)-TbH9-HTCC#1(161-392)

<400> 60

Met	His	His	His	His	His	His	Met	Ser	Arg	Ala	Phe	Ile	Ile	Asp	Pro
1				5					10					15	

Thr	Ile	Ser	Ala	Ile	Asp	Gly	Leu	Tyr	Asp	Leu	Leu	Gly	Ile	Gly	Ile
			20					25					30		

Pro	Asn	Gln	Gly	Gly	Ile	Leu	Tyr	Ser	Ser	Leu	Glu	Tyr	Phe	Glu	Lys
		35					40					45			

Ala	Leu	Glu	Glu	Leu	Ala	Ala	Ala	Phe	Pro	Gly	Asp	Gly	Trp	Leu	Gly
	50					55					60				

Ser	Ala	Ala	Asp	Lys	Tyr	Ala	Gly	Lys	Asn	Arg	Asn	His	Val	Asn	Phe	65	70	75	80
Phe	Gln	Glu	Leu	Ala	Asp	Leu	Asp	Arg	Gln	Leu	Ile	Ser	Leu	Ile	His	85	90	95	
Asp	Gln	Ala	Asn	Ala	Val	Gln	Thr	Thr	Arg	Asp	Ile	Leu	Glu	Gly	Ala	100	105	110	
Lys	Lys	Gly	Leu	Glu	Phe	Val	Arg	Pro	Val	Ala	Val	Asp	Leu	Thr	Tyr	115	120	125	
Ile	Pro	Val	Val	Gly	His	Ala	Leu	Ser	Ala	Ala	Phe	Gln	Ala	Pro	Phe	130	135	140	
Cys	Ala	Gly	Ala	Met	Ala	Val	Val	Gly	Gly	Ala	Leu	Lys	Leu	Met	Val	145	150	155	160
Asp	Phe	Gly	Ala	Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	165	170	175	
Gly	Pro	Gly	Ser	Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	180	185	190	
Val	Ala	Ser	Asp	Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	195	200	205	
Trp	Gly	Leu	Thr	Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	210	215	220	
Val	Ala	Ala	Ala	Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	225	230	235	240
Gln	Ala	Glu	Leu	Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	245	250	255	
Glu	Thr	Ala	Tyr	Gly	Leu	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	260	265	270	
Arg	Ala	Glu	Leu	Met	Ile	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	275	280	285	
Thr	Pro	Ala	Ile	Ala	Val	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	290	295	300	
Gln	Asp	Ala	Ala	Ala	Met	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	305	310	315	320
Thr	Ala	Thr	Leu	Leu	Pro	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	325	330	335	
Gly	Gly	Leu	Leu	Glu	Gln	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	340	345	350	
Ala	Ala	Ala	Asn	Gln	Leu	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	355	360	365	
Leu	Ala	Gln	Pro	Thr	Gln	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	370	375	380	

Leu	Trp	Lys	Thr	Val	Ser	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	385	390	395	400
Ser	Met	Ala	Asn	Asn	His	Met	Ser	Met	Thr	Asn	Ser	Gly	Val	Ser	Met	405	410	415	
Thr	Asn	Thr	Leu	Ser	Ser	Met	Leu	Lys	Gly	Phe	Ala	Pro	Ala	Ala	Ala	420	425	430	435
Ala	Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	440	445		
Ser	Leu	Gly	Ser	Ser	Leu	Gly	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Val	Ala	450	455	460	
Ala	Asn	Leu	Gly	Arg	Ala	Ala	Ser	Val	Gly	Ser	Leu	Ser	Val	Pro	Gln	465	470	475	480
Ala	Trp	Ala	Ala	Ala	Asn	Gln	Ala	Val	Thr	Pro	Ala	Ala	Arg	Ala	Leu	485	490	495	
Pro	Leu	Thr	Ser	Leu	Thr	Ser	Ala	Ala	Glu	Arg	Gly	Pro	Gly	Gln	Met	500	505	510	
Leu	Gly	Gly	Leu	Pro	Val	Gly	Gln	Met	Gly	Ala	Arg	Ala	Gly	Gly	Gly	515	520	525	
Leu	Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	530	535	540	
Ser	Pro	Ala	Ala	Gly	Lys	Leu	Thr	Gln	Leu	Leu	Lys	Leu	Leu	Ala	Lys	545	550	555	560
Leu	Ala	Glu	Leu	Val	Ala	Ala	Ala	Ile	Ala	Asp	Ile	Ile	Ser	Asp	Val	565	570	575	
Ala	Asp	Ile	Ile	Lys	Gly	Ile	Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	Thr	580	585	590	
Asn	Ala	Leu	Asn	Gly	Leu	Lys	Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	595	600	605	
Val	Thr	Gly	Leu	Phe	Ser	Arg	Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	610	615	620	
Ala	Gly	Val	Pro	Gly	Leu	Thr	Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	625	630	635	640
Thr	Gly	Leu	Phe	Gly	Ala	Ala	Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	645	650	655	
His	Ala	Asp	Ser	Leu	Ala	Ser	Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	660	665	670	
Ile	Gly	Gly	Gly	Ser	Gly	Phe	Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	675	680	685	
His	Ala	Ala	Ser	Thr	Arg	Gln	Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	690	695	700	

Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val Ser  
705 710 715 720

Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met  
725 730 735

His Pro Ser Ser Gly Ala Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser  
740 745 750

Glu Gly Ala Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu  
755 760 765

Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val Arg Asn Val Val  
770 775 780

<210> 61  
<211> 2445  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:fusion protein  
HTCC#1(184-392)-TbH9-HTCC#1(1-200)

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<221> CDS  
<222> (4) .. (2439)

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Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu  
20 25 30

aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct 144  
Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser  
35 40 45

cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg 192  
Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu  
50 55 60

acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg 240  
Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala  
65 70 75

gcc ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg 288  
Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala  
80 85 90 95

agc tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt 336  
Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly  
100 105 110

ttt ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg 384  
Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg  
115 120 125

cag gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag	432
Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu	
130 135 140	
cag gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt	480
Gln Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly	
145 150 155	
atg ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg	528
Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala	
160 165 170 175	
tcg aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc	576
Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly	
180 185 190	
act gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg	624
Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly	
195 200 205	
caa aag gtg ctg gta cga aac gtc gtc gaa ttc atg gtg gat ttc ggg	672
Gln Lys Val Leu Val Arg Asn Val Val Glu Phe Met Val Asp Phe Gly	
210 215 220	
gcg tta cca ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt	720
Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly	
225 230 235	
tcg gcc tcg ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt	768
Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser	
240 245 250 255	
gac ctg ttt tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg	816
Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu	
260 265 270	
acg gtg ggg tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg	864
Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala	
275 280 285	
gcc tcg ccg tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag	912
Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu	
290 295 300	
ctg acc gcc gcc cag gtc cgg gtt gct gcg gcg gcc tac gag acg gcg	960
Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala	
305 310 315	
tat ggg ctg acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa	1008
Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu	
320 325 330 335	
ctg atg att ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg	1056
Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala	
340 345 350	
atc gcg gtc aac gag gcc gaa tac ggc gag atg tgg gcc caa gac gcc	1104
Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala	
355 360 365	



gcc gcg atg ttt ggc tac gcc gcg gcg acg gcg acg gcg acg gcg acg	1152
Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr	
370 375 380	
ttg ctg ccg ttc gag gag gcg ccg gag atg acc agc gcg ggt ggg ctc	1200
Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu	
385 390 395	
ctc gag cag gcc gcc gcg gtc gag gag gcc tcc gac acc gcc gcg gcg	1248
Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala	
400 405 410 415	
aac cag ttg atg aac aat gtg ccc cag gcg ctg caa cag ctg gcc cag	1296
Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln	
420 425 430	
ccc acg cag ggc acc acg cct tct tcc aag ctg ggt ggc ctg tgg aag	1344
Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys	
435 440 445	
acg gtc tcg ccg cat cgg tcg ccg atc agc aac atg gtg tcg atg gcc	1392
Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala	
450 455 460	
aac aac cac atg tcg atg acc aac tcg ggt gtg tcg atg acc aac acc	1440
Asn Asn His Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr	
465 470 475	
ttg agc tcg atg ttg aag ggc ttt gct ccg gcg gcg gcc gcc cag gcc	1488
Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala	
480 485 490 495	
gtg caa acc gcg gcg caa aac ggg gtc cgg gcg atg agc tcg ctg ggc	1536
Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly	
500 505 510	
agc tcg ctg ggt tct tcg ggt ctg ggc ggt ggg gtg gcc gcc aac ttg	1584
Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu	
515 520 525	
ggt cgg gcg gcc tcg gtc ggt tcg ttg tcg gtg ccg cag gcc tgg gcc	1632
Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala	
530 535 540	
gcg gcc aac cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc	1680
Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr	
545 550 555	
agc ctg acc agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg	1728
Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly	
560 565 570 575	
ctg ccg gtg ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt	1776
Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly	
580 585 590	
gtg ctg cgt gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca	1824
Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala	
595 600 605	

gcc ggc gat atc atg agc aga gcg ttc atc atc gat cca acg atc agt Ala Gly Asp Ile Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser 610 615 620	1872
gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln 625 630 635	1920
ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu 640 645 650 655	1968
gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala 660 665 670	2016
gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu 675 680 685	2064
ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala 690 695 700	2112
aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly 705 710 715	2160
ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val 720 725 730 735	2208
gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly 740 745 750	2256
gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr 755 760 765	2304
ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu 770 775 780	2352
ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg gcg gac atc Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile 785 790 795	2400
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<210> 62

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:fusion protein  
HTCC#1(184-392)-TbH9-HTCC#1(1-200)

<400> 62

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Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	Thr	Asn	Ala	Leu	Asn	Gly	Leu	Lys
			20					25					30		
Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg
		35					40					45			
Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr
	50					55					60				
Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	Thr	Gly	Leu	Phe	Gly	Ala	Ala
65					70					75					80
Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	His	Ala	Asp	Ser	Leu	Ala	Ser
				85					90					95	
Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	Ile	Gly	Gly	Gly	Ser	Gly	Phe
			100					105					110		
Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	His	Ala	Ala	Ser	Thr	Arg	Gln
		115					120					125			
Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	Val	Gly	Ala	Ala	Ala	Glu	Gln
	130					135					140				
Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met
145					150					155					160
Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser
				165					170					175	
Lys	Gly	Thr	Thr	Thr	Lys	Lys	Tyr	Ser	Glu	Gly	Ala	Ala	Ala	Gly	Thr
			180					185					190		
Glu	Asp	Ala	Glu	Arg	Ala	Pro	Val	Glu	Ala	Asp	Ala	Gly	Gly	Gly	Gln
	195						200					205			
Lys	Val	Leu	Val	Arg	Asn	Val	Val	Glu	Phe	Met	Val	Asp	Phe	Gly	Ala
	210				215						220				
Leu	Pro	Pro	Glu	Ile	Asn	Ser	Ala	Arg	Met	Tyr	Ala	Gly	Pro	Gly	Ser
225					230					235					240
Ala	Ser	Leu	Val	Ala	Ala	Ala	Gln	Met	Trp	Asp	Ser	Val	Ala	Ser	Asp
				245					250					255	
Leu	Phe	Ser	Ala	Ala	Ser	Ala	Phe	Gln	Ser	Val	Val	Trp	Gly	Leu	Thr
			260					265					270		
Val	Gly	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val	Ala	Ala	Ala
		275					280					285			
Ser	Pro	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu
	290					295					300				
Thr	Ala	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr
305					310					315					320



Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu  
                                 645                                650                                655  
 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp  
                                 660                                665                                670  
 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu  
                                 675                                680                                685  
 Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn  
                                 690                                695                                700  
 Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu  
                                 705                                710                                715                                720  
 Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val  
                                 725                                730                                735  
 Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala  
                                 740                                745                                750  
 Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu  
                                 755                                760                                765  
 Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu  
                                 770                                775                                780  
 Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile  
                                 785                                790                                795                                800  
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<210> 63  
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 <212> DNA  
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<220>  
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           TbRa12-HTCC#1

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 ctg tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg   96  
 Leu Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met  
                                 20                                25                                30  
 gcg atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat   144  
 Ala Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His  
                                 35                                40                                45

atc ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc	192
Ile Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly	
50 55 60	
aac ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt	240
Asn Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser	
65 70 75	
ctc ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg	288
Leu Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro	
80 85 90 95	
atc aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc	336
Ile Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro	
100 105 110	
ggg gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt	384
Gly Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg	
115 120 125	
aca ggg aac gtg aca ttg gcc gag gga ccc ccg gcc gaa ttc cta gta	432
Thr Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Leu Val	
130 135 140	
cct aga ggt tca atg agc aga gcg ttc atc atc gat cca acg atc agt	480
Pro Arg Gly Ser Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser	
145 150 155	
gcc att gac ggc ttg tac gac ctt ctg ggg att gga ata ccc aac caa	528
Ala Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln	
160 165 170 175	
ggg ggt atc ctt tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag	576
Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu	
180 185 190	
gag ctg gca gca gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg	624
Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala	
195 200 205	
gac aaa tac gcc ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa	672
Asp Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu	
210 215 220	
ctg gca gac ctc gat cgt cag ctc atc agc ctg atc cac gac cag gcc	720
Leu Ala Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala	
225 230 235	
aac gcg gtc cag acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt	768
Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly	
240 245 250 255	
ctc gag ttc gtg cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc	816
Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val	
260 265 270	
gtc ggg cac gcc cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc	864
Val Gly His Ala Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly	
275 280 285	

gcg atg gcc gta gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg	912
Ala Met Ala Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr	
290 295 300	
ctg atc aac gcg act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag	960
Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu	
305 310 315	
ttg gtc gcg gcc gcc att gcg gac atc att tcg gat gtg gcg gac atc	1008
Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile	
320 325 330 335	
atc aag ggc atc ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc	1056
Ile Lys Gly Ile Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu	
340 345 350	
aac ggc ctg aaa gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga	1104
Asn Gly Leu Lys Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly	
355 360 365	
ctg ttc tct cga ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc	1152
Leu Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val	
370 375 380	
ccc ggc ttg acc ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg	1200
Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu	
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Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp	
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Ser Leu Ala Ser Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly	
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Gly Ser Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala	
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Ser Gln Gly Met Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser	
480 485 490 495	
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Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala	
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 Asn Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly  
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 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala Glu Phe Leu Val Pro  
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 Arg Gly Ser Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala  
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 Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu  
           180                          185                          190  
 Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp  
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 Lys Tyr Ala Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu  
           210                          215                          220  
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<211> 8794

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:vector encoding  
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<400> 91

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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:region encoding  
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:vector encoding  
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 <223> Description of Artificial Sequence:nucleic acid  
 sequence of HTCC#1 peptide 28 for T-cell epitope  
 mapping  
  
 <400> 121  
 tcgaaagga cgacgacgaa gaagtactcg gaaggcgcgg cggcgggcac tgaagacgcc 60  
  
 <210> 122  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:nucleic acid  
 sequence of HTCC#1 peptide 29 for T-cell epitope  
 mapping  
  
 <400> 122  
 gcggcgggca ctgaagacgc cgagcgcgcg ccagtcgaag ctgacgcggg cgggtgggcaa 60  
  
 <210> 123  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence



<220>  
 <223> Description of Artificial Sequence:nucleic acid  
 sequence of HTCC#1 peptide 30 for T-cell epitope  
 mapping

<400> 123  
 cgcgcgccag tcgaagctga cgcgggcggt gggcaaaagg tgctggtacg aaacgtcgtc 60

<210> 124  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
 1 for T-cell epitope mapping

<400> 124  
 Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly  
 1 5 10 15  
 Leu Tyr Asp Leu  
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<210> 125  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
 2 for T-cell epitope mapping

<400> 125  
 Ile Asp Gly Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly  
 1 5 10 15  
 Gly Ile Leu Tyr  
 20

<210> 126  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
 3 for T-cell epitope mapping

<400> 126  
 Asn Gln Gly Gly Ile Leu Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala  
 1 5 10 15  
 Leu Glu Glu Leu  
 20

<210> 127  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
4 for T-cell epitope mapping

<400> 127  
Glu Lys Ala Leu Glu Glu Leu Ala Ala Ala Phe Pro Gly Asp Gly Trp  
1 5 10 15  
Leu Gly Ser Ala .  
20

<210> 128  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
5 for T-cell epitope mapping

<400> 128  
Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala Gly Lys Asn Arg  
1 5 10 15  
Asn His Val Asn  
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<210> 129  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
6 for T-cell epitope mapping

<400> 129  
Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu Asp  
1 5 10 15  
Arg Gln Leu Ile  
20

<210> 130  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
7 for T-cell epitope mapping

<400> 130  
 Asp Leu Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala  
 1 5 10 15

Val Gln Thr Thr  
 20

<210> 131  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
 8 for T-cell epitope mapping

<400> 131  
 Ala Asn Ala Val Gln Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys  
 1 5 10 15

Gly Leu Glu Phe  
 20

<210> 132  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
 9 for T-cell epitope mapping

<400> 132  
 Ala Lys Lys Gly Leu Glu Phe Val Arg Pro Val Ala Val Asp Leu Thr  
 1 5 10 15

Tyr Ile Pro Val  
 20

<210> 133  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
 10 for T-cell epitope mapping

<400> 133  
 Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala Leu Ser Ala Ala Phe  
 1 5 10 15

Gln Ala Pro Phe  
 20

<210> 134  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
11 for T-cell epitope mapping

<400> 134  
Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val Val Gly  
1 5 10 15  
Gly Ala Leu Ala  
20

<210> 135  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
12 for T-cell epitope mapping

<400> 135  
Val Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn  
1 5 10 15  
Ala Thr Gln Leu  
20

<210> 136  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
13 for T-cell epitope mapping

<400> 136  
Leu Ile Asn Ala Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu  
1 5 10 15  
Leu Val Ala Ala  
20

<210> 137  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
14 for T-cell epitope mapping

<400> 137  
 Leu Ala Glu Leu Val Ala Ala Ala Ile Ala Asp Ile Ile Ser Asp Val  
     1                    5                    10                    15  
 Ala Asp Ile Ile  
                     20

<210> 138  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
       15 for T-cell epitope mapping

<400> 138  
 Ser Asp Val Ala Asp Ile Ile Lys Gly Ile Leu Gly Glu Val Trp Glu  
     1                    5                    10                    15  
 Phe Ile Thr Asn  
                     20

<210> 139  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
       16 for T-cell epitope mapping

<400> 139  
 Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys Glu Leu Trp  
     1                    5                    10                    15  
 Asp Lys Leu Thr  
                     20

<210> 140  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
       17 for T-cell epitope mapping

<400> 140  
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg  
     1                    5                    10                    15  
 Gly Trp Ser Asn  
                     20

<210> 141  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
       18 for T-cell epitope mapping  
  
 <400> 141  
 Phe Ser Arg Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro  
   1                  5                  10                  15  
  
 Gly Leu Thr Gly  
                   20

<210> 142  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
       19 for T-cell epitope mapping  
  
 <400> 142  
 Gly Val Pro Gly Leu Thr Gly Ala Thr Ser Gly Leu Ser Gln Val Thr  
   1                  5                  10                  15  
  
 Gly Leu Phe Gly  
                   20

<210> 143  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
       20 for T-cell epitope mapping  
  
 <400> 143  
 Gln Val Thr Gly Leu Phe Gly Ala Ala Gly Leu Ser Ala Ser Ser Gly  
   1                  5                  10                  15  
  
 Leu Ala His Ala  
                   20

<210> 144  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
       21 for T-cell epitope mapping

<400> 144

Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser Ser Ala Ser Leu  
1 5 10 15

Pro Ala Leu Ala  
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<210> 145

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide  
22 for T-cell epitope mapping

<400> 145

Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe Gly  
1 5 10 15

Gly Leu Pro Ser  
20

<210> 146

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide  
23 for T-cell epitope mapping

<400> 146

Gly Phe Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr  
1 5 10 15

Arg Gln Ala Leu  
20

<210> 147

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:HTCC#1 peptide  
24 for T-cell epitope mapping

<400> 147

Ala Ser Thr Arg Gln Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly  
1 5 10 15

Ala Ala Ala Glu  
20

<210> 148  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
25 for T-cell epitope mapping

<400> 148  
Pro Val Gly Ala Ala Ala Glu Gln Val Gly Gly Gln Ser Gln Leu Val  
1 5 10 15  
Ser Ala Gln Gly  
20

<210> 149  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
26 for T-cell epitope mapping

<400> 149  
Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met Gly Gly Pro Val Gly  
1 5 10 15  
Met Gly Gly

<210> 150  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
27 for T-cell epitope mapping

<400> 150  
Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser Lys Gly  
1 5 10 15  
Thr Thr Thr Lys  
20

<210> 151  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:HTCC#1 peptide  
28 for T-cell epitope mapping



<400> 151  
 Ser Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly  
           1                          5                          10                          15

Thr Glu Asp Ala  
                   20

<210> 152  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
           29 for T-cell epitope mapping

<400> 152  
 Ala Ala Gly Thr Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala  
           1                          5                          10                          15

Gly Gly Gly Gln  
                   20

<210> 153  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:HTCC#1 peptide  
           30 for T-cell epitope mapping

<400> 153  
 Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln Lys Val Leu Val  
           1                          5                          10                          15

Arg Asn Val Val  
                   20

<210> 154  
 <211> 84  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<220>  
 <223> secreted form of DPPD

<400> 154  
 Asp Pro Pro Asp Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro  
           1                          5                          10                          15

Gly Gly Arg Trp Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys  
           20                          25                          30

Tyr Pro Asp Gly Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr  
           35                          40                          45

Gly Pro Gln Phe Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro  
 50 55 60

Gly Pro Pro Pro Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln  
 65 70 75 80

Pro Asn Ala Pro

<210> 155  
 <211> 2836  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <223> Mtb9.9A (MTI-A)

<220>  
 <221> modified\_base  
 <222> (1)..(2836)  
 <223> n = g, a, c or t

<400> 155  
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 gggtgcgtcg gtcagctggc cgaatcccaa tgattggtgg ctcngtgcgg ttgctgggct 120  
 cgattacccc cacggaaagg acgacgatcg ttcgtttgct cggtcagtcg tacttggcga 180  
 cgggcatggc gcggtttctt acctcgatcg cacagcagct gaccttcggc ccagggggca 240  
 caacggctgg ctccggcgga gcctggtacc caacgccaca attcgccggc ctgggtgcag 300  
 gcccgcggtt gtcggcgagt ttggcgcggg cggagccggt cgggaggttg tcggtgccgc 360  
 caagttgggc gtcgcggct cggccttcg cggagaagcc tgaggcgggc acgccgatgt 420  
 ccgtcatcgg cgaagcgtcc agctgcggtc agggaggcct gcttcgaggc ataccgctgg 480  
 cgagagcggg gcggcgta ca ggcgccttcg ctaccgata cgggttcgc cacagcgtga 540  
 ttaccgggtc tccgtcggcg ggatagcttt cgatccggtc tgcgcggccg ccggaaatgc 600  
 tgcagatagc gatcgaccgc gccggtcggg aaacgccgca caccgcacta tcaatgcgca 660  
 cggcgggcgt tgatgcaaaa ttgaccgtcc cgacggggct ttatctgcgg caagatttca 720  
 tccccagccc ggtcgggtgg ccgataaata cgctgggtcag cgcgactctt ccggctgaat 780  
 tcgatgctct gggcgccccg tcgacgccga gtatctcgag tgggccgcaa acccggtcaa 840  
 acgtgtttac tgtggcggtt ccacagggtga atttgcggtg ccaactggtg aacacttgcg 900  
 aacgggtggc atcgaaatca acttggttgc gatgtgagc ctactctctt gcagagagcc 960  
 gttgctggga ttaattggga gaggaagaca gcatgtcgtt cgtgaccaca cagccggaag 1020  
 ccctggcagc tgcggcgggc aacctacagg gtattggcac gacaatgaac gcccagaacg 1080  
 cggccgcggc tgcctcaacc accggagtag tgcccgagc cgccgatgaa gtatcagcgc 1140  
 tgaccgcggc tcagtttgct gcgcacgcgc agatgtacca aacggtcagc gcccaggccg 1200  
 cggccattca cgaaatgttc gtgaacacgc tgggtggccag ttctgggtca tacgcggcca 1260  
 ccgaggcggc caacgcagcc gctgccggct gaacgggctc gcacgaacct gctgaaggag 1320  
 agggggaaca tccggagttc tcgggtcagg ggttgcgcca gcgccagcc gattcagcta 1380  
 tcggcgctca taacagcaga cgatctaggc attcagtact aaggagacag gcaacatggc 1440  
 ctacggtttt atgacggatc cgcattgcgt gcgggacatg gcgggcccgt ttgaggtgca 1500  
 cgcccagacg gtggaggacg aggtcgcggc gctgtggggc tccgcgcaaa acatttccgg 1560  
 tgcgggctgg agtggcatgg ccgaggcgac ctgcgtagac accatgacct agatgaatca 1620  
 ggcgtttcgc aacatcgtga acatgctgca cggggtgctg gacgggctgg ttgcgcagc 1680  
 caacaactac gaacagcaag agcaggcctc ccagcagatc ctgagcagct agcgccgaaa 1740  
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 ttcggggacg tcgacgctca tggcgccatg atccgcgctc aggcggcgct gcttgaggcg 1860  
 gagcatcagg ccacgttcg tgatgtgttg gccgcgggtg acttttgggg cggcgcgggt 1920  
 tcggtggctt gccaggagt cattaccag ttgggcgcta acttccaggt gatctacgag 1980  
 caggccaacg cccacgggca gaaggtgcag gctgcggca acaacatggc gcaaaccgac 2040  
 agcgccgtcg gctccagctg ggcctaaaac tgaacttcag tcgcggcagc acaccaacca 2100  
 gccggtgtgc tgctgtgtcc tgcagttaac tagcactcga ccgctgaggt agcgatggat 2160  
 caacagagta cccgcaccga catcaccgtc aacgtcgacg gcttctggat gcttcaggcg 2220  
 ctactggata tccgccacgt tgcgcctgag ttacgttgcc ggccgtacgt ctccaccgat 2280

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tccaatgact ggctaaacga gcacccgggg atggcggtca tgcgcgagca gggcattgtc 2340
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cttgaagtgc tgcacctgct gtcacgcggc aagttgctgt acgggggtcat agacgacgag 2460
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attcggcacg aggcacgagg cgggtgctggt gacgacggga tcgatcacga tcatcgaccg 2760
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ccatgggttc ttcccg                                     2836

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<210> 156
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
      ORF peptide

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<400> 156
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala
  1             5             10             15

```

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<210> 157
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
      ORF peptide

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```

<400> 157
Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
  1             5             10             15

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```

<210> 158
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:MtB9.9A (MTI-A)
      ORF peptide

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<400> 158
Asp Ala His Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu
  1             5             10             15

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<210> 159
<211> 15
<212> PRT
<213> Artificial Sequence

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<220>  
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
 ORF peptide

<400> 159  
 Met Ile Arg Ala Gln Ala Ala Ser Leu Glu Ala Glu His Gln Ala  
 1 5 10 15

<210> 160  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
 ORF peptide

<400> 160  
 Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val  
 1 5 10 15

<210> 161  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
 ORF peptide

<400> 161  
 Ala Glu His Gln Ala Ile Val Arg Asp Val Leu Ala Ala Gly Asp  
 1 5 10 15

<210> 162  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
 ORF peptide

<400> 162  
 Ile Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala  
 1 5 10 15

<210> 163  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
 ORF peptide

<400> 163

Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln  
1 5 10 15

<210> 164

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
ORF peptide

<400> 164

Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe Ile Thr  
1 5 10 15

<210> 165

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
ORF peptide

<400> 165

Gly Ser Val Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn  
1 5 10 15

<210> 166

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
ORF peptide

<400> 166

Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu  
1 5 10 15

Gln Ala

<210> 167

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
ORF peptide

<400> 167

Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala Asn Ala His Gly Gln  
1 5 10 15

<210> 168

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
ORF peptide

<400> 168

Ile Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala  
1 5 10 15

<210> 169

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
ORF peptide

<400> 169

Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala  
1 5 10 15

<210> 170

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
ORF peptide

<400> 170

Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala  
1 5 10 15

<210> 171

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:MtB9.9A (MTI-A)  
ORF peptide

<400> 171

Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala  
1 5 10 15

<210> 172  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Mtb9.8 ORF  
peptide

<400> 172  
Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln  
1 5 10 15

<210> 173  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Mtb9.8 ORF  
peptide

<400> 173  
Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala  
1 5 10 15

<210> 174  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Mtb9.8 ORF  
peptide

<400> 174  
Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met  
1 5 10 15

<210> 175  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Mtb9.8 ORF  
peptide

<400> 175  
Ser Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly  
1 5 10 15

<210> 176  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Mtb9.8 ORF  
 peptide  
 <400> 176  
 Lys Ala Gly Leu Met His Thr Ile Gly Gln Ala Glu Gln Ala  
 1 5 10

<210> 177  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Mtb9.8 ORF  
 peptide  
 <400> 177  
 Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln  
 1 5 10 15

<210> 178  
 <211> 15  
 <212> PRT  
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<220>  
 <223> Description of Artificial Sequence:Mtb9.8 ORF  
 peptide  
 <400> 178  
 Gln Ala Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly  
 1 5 10 15

<210> 179  
 <211> 15  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Mtb9.8 ORF  
 peptide  
 <400> 179  
 Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala  
 1 5 10 15

<210> 180  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Mtb9.8 ORF  
 peptide



<400> 180  
 Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His  
           1                  5                  10                  15

<210> 181  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Mtb9.8 ORF  
           peptide

<400> 181  
 Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala  
           1                  5                  10                  15

<210> 182  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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           peptide

<400> 182  
 Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val  
           1                  5                  10                  15

<210> 183  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Mtb9.8 ORF  
           peptide

<400> 183  
 Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu Leu Asp  
           1                  5                  10                  15

<210> 184  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Mtb9.8 ORF  
           peptide

<400> 184  
 Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn  
           1                  5                  10                  15

<210> 185  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Mtb9.8 ORF  
peptide

<400> 185  
Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala  
1 5 10 15

<210> 186  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Mtb9.8 ORF  
peptide

<400> 186  
Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala  
1 5 10 15

Asp Ala

<210> 187  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR  
amplification primer PDM-294

<400> 187  
cgtaatcacg tgcagaagta cggcggatc 29

<210> 188  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:PCR  
amplification primer PDM-295

<400> 188  
ccgactagaa ttcactattg. acaggcccat c 31

<210> 189  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PCR  
 amplification primer PDM-268  
  
 <400> 189  
 ctaagtagta ctgatcggt gtcggtgggc 30  
  
 <210> 190  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 amplification primer PDM-296  
  
 <400> 190  
 catcgatagg cctggccgca tcgtcacc 28  
  
 <210> 191  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 amplification primer PDM-157  
  
 <400> 191  
 ctagttagta ctcagtcgca gaccgtg 27  
  
 <210> 192  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 amplification primer PDM-160  
  
 <400> 192  
 gcagtgcga attcacttcg actcc 25  
  
 <210> 193  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 amplification primer PDM-69  
  
 <400> 193  
 ggatccagcg ctgagatgaa gaccgatgcc gct 33

<210> 194  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 amplification primer PDM-83  
  
 <400> 194  
 ggatatctgc agaattcagg tttaaagccc atttgcca 38  
  
 <210> 195  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 amplification primer PDM-192  
  
 <400> 195  
 tgtggctcga aaccaccgag cggttc 26  
  
 <210> 196  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 amplification primer PDM-60  
  
 <400> 196  
 gagagaattc tcagaagccc atttgcgagg aca 33  
  
 <210> 197  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 oligonucleotide 5' primer  
  
 <400> 197  
 caattacata tgcataacca tcaccatcac atgagcagag cgttcatcat c 51  
  
 <210> 198  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence:PCR  
 oligonucleotide 3' primer

<400> 198  
 catggaattc gccgttagac gacgtttcgt a 31

<210> 199  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PCR  
 amplification oligonucleotide 5' primer

<400> 199  
 caattacata tgcatacaca tcaccatcac acggccgcgt ccgataactt c 51

<210> 200  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:PCR  
 amplification oligonucleotide 3' primer

<400> 200  
 ctaatcgaat tcggccgggg gtccctcggc caa 33

<210> 201  
 <211> 1179  
 <212> DNA  
 <213> Mycobacterium tuberculosis

<220>  
 <221> CDS  
 <222> (1)..(1179)  
 <223> HTCC#1

<400> 201  
 atg agc aga gcg ttc atc atc gat cca acg atc agt gcc att gac ggc 48  
 Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly  
 1 5 10 15

ttg tac gac ctt ctg ggg att gga ata ccc aac caa ggg ggt atc ctt 96  
 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu  
 20 25 30

tac tcc tca cta gag tac ttc gaa aaa gcc ctg gag gag ctg gca gca 144  
 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala  
 35 40 45

gcg ttt ccg ggt gat ggc tgg tta ggt tcg gcc gcg gac aaa tac gcc 192  
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala  
 50 55 60

ggc aaa aac cgc aac cac gtg aat ttt ttc cag gaa ctg gca gac ctc 240  
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu  
 65 70 75 80

gat cgt cag ctc atc agc ctg atc cac gac cag gcc aac gcg gtc cag	288
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln	
85 90 95	
acg acc cgc gac atc ctg gag ggc gcc aag aaa ggt ctc gag ttc gtg	336
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val	
100 105 110	
cgc ccg gtg gct gtg gac ctg acc tac atc ccg gtc gtc ggg cac gcc	384
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala	
115 120 125	
cta tcg gcc gcc ttc cag gcg ccg ttt tgc gcg ggc gcg atg gcc gta	432
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val	
130 135 140	
gtg ggc ggc gcg ctt gcc tac ttg gtc gtg aaa acg ctg atc aac gcg	480
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala	
145 150 155 160	
act caa ctc ctc aaa ttg ctt gcc aaa ttg gcg gag ttg gtc gcg gcc	528
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala	
165 170 175	
gcc att gcg gac atc att tcg gat gtg gcg gac atc atc aag ggc atc	576
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile	
180 185 190	
ctc gga gaa gtg tgg gag ttc atc aca aac gcg ctc aac ggc ctg aaa	624
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys	
195 200 205	
gag ctt tgg gac aag ctc acg ggg tgg gtg acc gga ctg ttc tct cga	672
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg	
210 215 220	
ggg tgg tcg aac ctg gag tcc ttc ttt gcg ggc gtc ccc ggc ttg acc	720
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr	
225 230 235 240	
ggc gcg acc agc ggc ttg tcg caa gtg act ggc ttg ttc ggt gcg gcc	768
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala	
245 250 255	
ggt ctg tcc gca tcg tcg ggc ttg gct cac gcg gat agc ctg gcg agc	816
Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser	
260 265 270	
tca gcc agc ttg ccc gcc ctg gcc ggc att ggg ggc ggg tcc ggt ttt	864
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe	
275 280 285	
ggg ggc ttg ccg agc ctg gct cag gtc cat gcc gcc tca act cgg cag	912
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln	
290 295 300	
gcg cta cgg ccc cga gct gat ggc ccg gtc ggc gcc gct gcc gag cag	960
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln	
305 310 315 320	

gtc ggc ggg cag tcg cag ctg gtc tcc gcg cag ggt tcc caa ggt atg 1008  
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met  
 325 330 335

ggc gga ccc gta ggc atg ggc ggc atg cac ccc tct tcg ggg gcg tcg 1056  
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser  
 340 345 350

aaa ggg acg acg acg aag aag tac tcg gaa ggc gcg gcg gcg ggc act 1104  
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr  
 355 360 365

gaa gac gcc gag cgc gcg cca gtc gaa gct gac gcg ggc ggt ggg caa 1152  
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln  
 370 375 380

aag gtg ctg gta cga aac gtc gtc taa 1179  
 Lys Val Leu Val Arg Asn Val Val  
 385 390

<210> 202  
 <211> 392  
 <212> PRT  
 <213> Mycobacterium tuberculosis

<400> 202  
 Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly  
 1 5 10 15  
 Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu  
 20 25 30  
 Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala  
 35 40 45  
 Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala  
 50 55 60  
 Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu  
 65 70 75 80  
 Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln  
 85 90 95  
 Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val  
 100 105 110  
 Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala  
 115 120 125  
 Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val  
 130 135 140  
 Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala  
 145 150 155 160  
 Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala  
 165 170 175

Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Ile  
 180 185 190  
 Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys  
 195 200 205  
 Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg  
 210 215 220  
 Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr  
 225 230 235 240  
 Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala  
 245 250 255  
 Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser  
 260 265 270  
 Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe  
 275 280 285  
 Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln  
 290 295 300  
 Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Glu Gln  
 305 310 315 320  
 Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met  
 325 330 335  
 Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser  
 340 345 350  
 Lys Gly Thr Thr Thr Lys Lys Tyr Ser Glu Gly Ala Ala Ala Gly Thr  
 355 360 365  
 Glu Asp Ala Glu Arg Ala Pro Val Glu Ala Asp Ala Gly Gly Gly Gln  
 370 375 380  
 Lys Val Leu Val Arg Asn Val Val  
 385 390